

1 31
TCG ACT ATG AAT GAT AAT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

Cadherin

|xx EC motif xx|

FIG. 1 (1 of 5)

FIG. 1 (1 of 5)

901 931
 AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

 961 991
 ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

 1021 1051
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

 1081 1111
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

 1141 1171
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
 lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

 1201 1231
 GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
 val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

 1261 1291
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
 tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

 1321 1351
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

 1381 1411
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

 1441 1471
 CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
 pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

 1501 1531
 GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
 val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

 1561 1591
 GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
 ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

 1621 |xxxxxxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxx
 AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
 lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

 xxxxxxxxxxxxxxxxxxxxxxxxxxxx| 1711
 TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

 1741 1771
 AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
 ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

 1801 1831
 TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
 ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

FIG. 1 (2 of 5)

1861 1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 |xxxxxx ITAM xxxxx| 2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101 2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221 2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491 |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731 |xxxxxxxxxxxxx
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AAC AAG CGT CTC ATC ACG GCA CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

FIG. 1 (3 of 5)

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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881                                2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941                                2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

3001                                3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

3061                                3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

3121                                3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181                                3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241                                3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301                                3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361                                3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421                                3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481                                3511
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541                                3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601                                3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661                                3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721                                3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3781                                3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3841                                3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901                                3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961                                3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

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FIG. 1 (4 of 5)

4021
AAC TCG

4021
AAC TCG

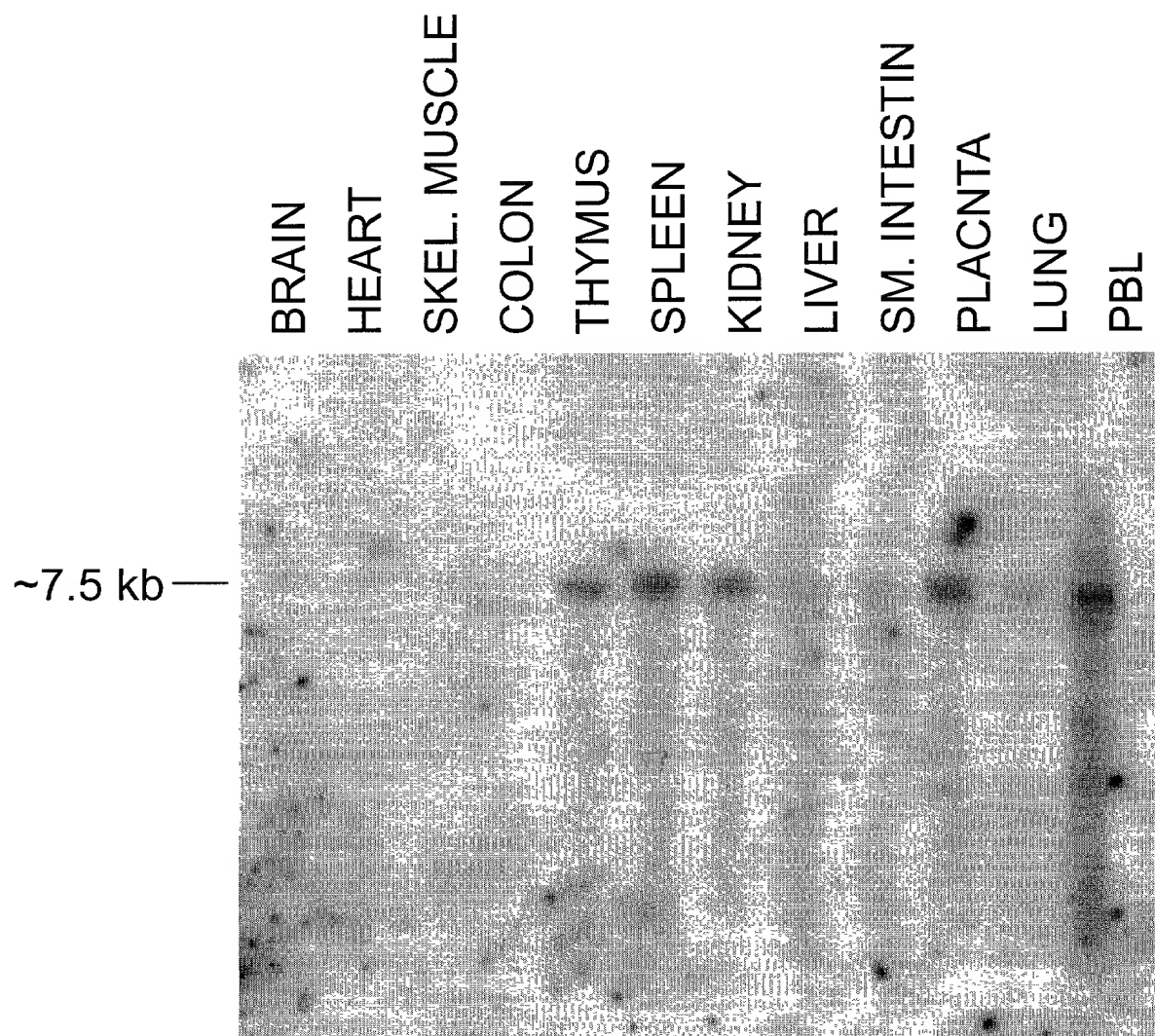
[illegible]

FIG. 2A

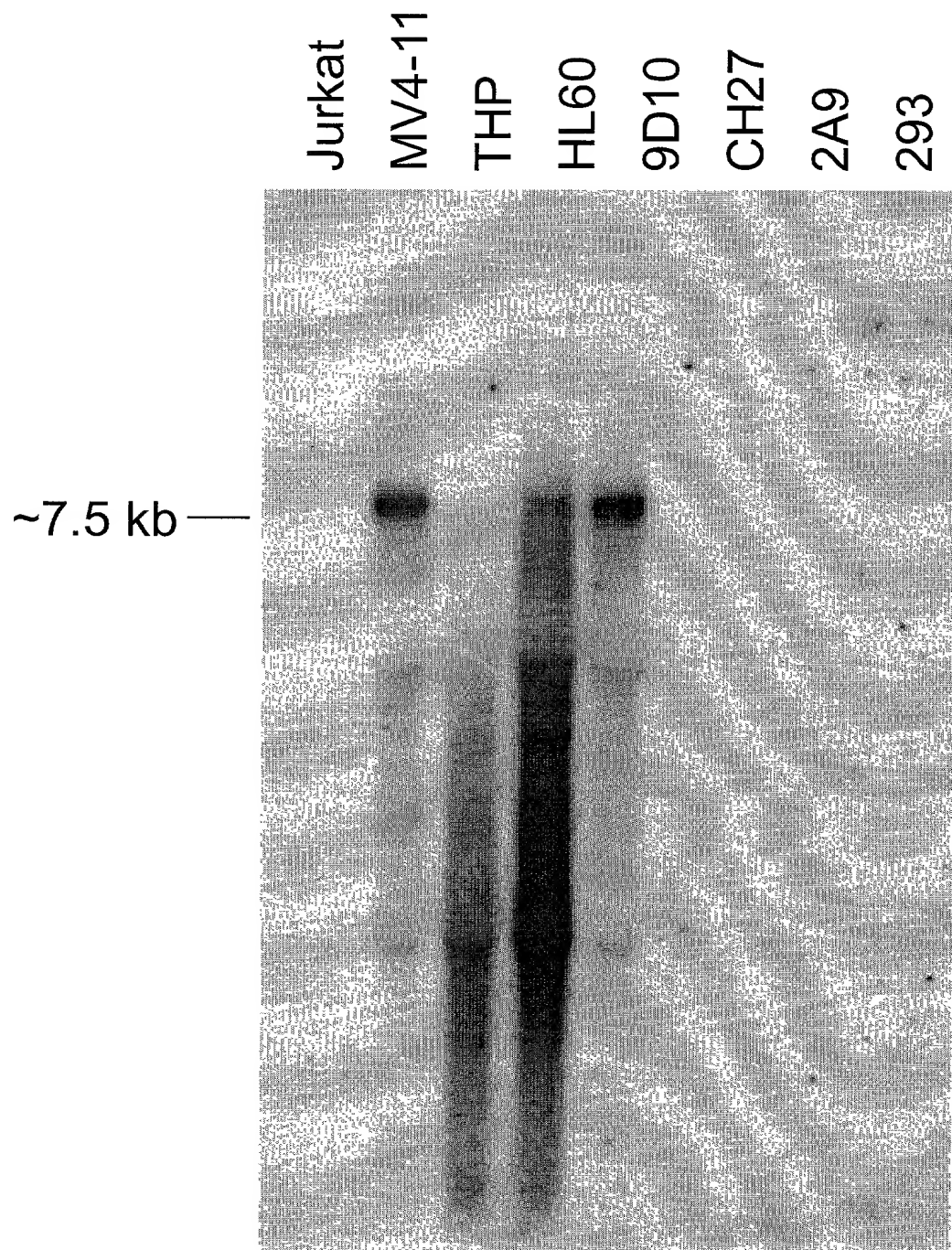


FIG. 2B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFEYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYPELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
KIAA	PVSANLPSGYLGYPELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 3A (1 of 5)

HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P ---- T K K L F H E E L A L Q W V V C S G -- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L P R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M ---- A F A K P K L Q R ----- V Q D S N L ---- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E S ----- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S I L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G I L L R E V G T A L Q E F R E ---- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G I L L R E V G T A L Q E F R E ---- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G I L L R E T S I A L Q D N Y E ---- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D ---- V R H L A L A V L K N L M A K H S F D D R Y E R P R K Q A Q I A S
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A A M P N S A S R D E F P C G ---- F T S P -- A N -- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E ----- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E ----- G A --- G A I T

FIG. 3A (2 of 5)

HC2A	KDLLGAISGSIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
KIAA	KDLLGAISGSIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGKREDSRGSLIP-EGATGFPDQGNLTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI PRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
HC1	QNFRYLQKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGKH
HC3	SCFEYKGGKVFERNMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGERGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQREALISGNLATEAH
HC2A	LTALDITLSLFTLAFKNQLLADHGHNPLMKKVFVDVYLCFLQKHQSEALKNVFTALRS LIY
KIAA	LTALDITLSLFTLAFKNQLLADHGHNPLMKKVFVDVYLCFLQKHQSEALKNVFTALRS LIY
rat	-----KLSRGHSPLMKKVFVDVYLCFLQKHQSEALKNVFTALRS LIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
KIAA	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
rat	KFPSTFYEGRADMCALCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCCTSKI STRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNF EIGN--NFARVK
HC5	KFGDLLFEEEEVEQCFDLCHQVLHHCSSSMDVTRS QACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKD LTKRI RTVLM
KIAA	LQVIISVSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKD LTKRI RTVLM
rat	LQVIISLSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKD LTKRI RTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKD LTKRI RTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKN SNFPAEVKD LTKRI RTVLM
HC3	MQVPMSLSSLVGT SQNFNEEFLRRSLK TILTYAEEDLELRETTFPDQVQDLVFNLMHILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PFPTQVEELLCNLNSILY

FIG. 3A (3 of 5)

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		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDL	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDL	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDL	LSEAAMCYVHV
HC4	ATAQMKEHEKDPPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGDL	FSEAAMCYVHV
HC1	ATAQMKEHEKDPPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDL	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAKGHSERSNHAEAAQCLVHS	
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLTLWLQNMAEKHTKKKCYTEAMCLVHA	
	SH3	
HC2A	TALVAEYLTRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLPHSHSACLRSSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYLKRKGYWKVEKICTASLLSEDTHPCDNSNLLTTPSGGSMFSGMWPFLSITPN	
HC3	AALVAEYLSMLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLED-----	HSYLPVGSVSFQNISSN
	ITAM	
HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPIPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELQCVNGLWKAERYETIIEISKLGPI
HC1	KEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVLPIPI	
HC5	VLEESVVSSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPIPI	
	ITAM ITAM ITAM ITAM	
HC2A	YEKRRD-----	
KIAA	YEKRRDFERLAHLDYTLHRAYSKVTVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETTHTLYDLTHRPYSKVTETVITR-----	AAGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG-----	TFERVAFYGGQ
HC1	FEKQRDFKKLSDLYYDIHRSYLVKVAEVDNSEKRLFG-----	RYRVAFYGGQ
HC3	HEANRDAKKLSTIHGKLQEAFAFSKIVHQSTGWERMFG-----	TYFRVGFYGGQ
HC5	LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG-----	TYFRVGFYGGQ
	ITAM ITAM	
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEDDGKEYIYKEPKLTGLSEISRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA	
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLLLKLYADKFGADNVKIIQDSKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDPCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCQCFGAEFVEVIKDSNPVDPCKLDPNKA	
	ITAM	
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
HC4	HIQVTVYVKPYFDDKELTERKTEFERHNISRFVFEAPYTLGSKKQGCIEEQCKRRTILT	
HC1	YIQVTVYVTPFFEEKEIEDRKTDFFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT	
HC3	YIQITVVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKRTILT	
HC5	YIQITVVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT	
Y		

FIG. 3A (4 of 5)

		Coiled-Coil 1
HC2A	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFFPYVKKRIPINCEQQINLKP	EDGATDEIKDKTAEQLKLCSSSTDVDMIQLQLKLQGSV
HC1	SHLFFPYVKKRIQVISQSSTELNP	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPIKTRVNVTHKEEIIILTP	IEVAIEDMQKKTQELAFATHQDPADPKMLQMLVQGSV
HC5	MHAFPIKTRISVIQKEEFVLTP	IEVAIEDMKKKTLQLAVAINQEPDAKMLQMLVQGSV
		Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE	
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE	
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE	
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSIALLNERLIKEDQVE	
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE	
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRNKNSLIGPVQKE	
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE	
		Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVE	RICPGEDKRATKFPAPHLQRHQRTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILQEDTMHSPWMSNTLHVFCALSGTSSDRGYGSPRYA
HC1	YQEELRSHYKDLSELSTVMNE	QITGRDDLK---RGVDQTCTRVISKATPALPTVSIS
HC3	YQRELG---KLSS-----	--P-----
HC5	YQQLKKNYNKLKENLRPMIER	KIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--
		PBM
HC2A	SSVV-----	
KIAA	-----	
rat	CVTLPHPEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWTVIFNSRFYRSWGK	
HC4	EV-----	
HC1	SAEV-----	
HC3	-----	
HC5	-----	
HC2A	-----	
KIAA	-----	
rat	VHIFF-----	
HC4	-----	
HC1	-----	
HC3	-----	
HC5	-----	

FIG. 3A (5 of 5)

A		B		C		D		E	
CLASP-1	YRVAFYQG:::GFFEEE	EGKEYIYKEP							
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDE	DGKEYIYKEP							
CLASP-2		FEDEDGKEYIYKEP							
CLASP-6	FRVAFFGQ:::GFFEDE	DGKEYIYKEP							
CLASP-4	FRVAFYQG:::SFFEEE	DGKEYIYKEP							
DOCK180	FAVGYYQG:::GFPTFLRGKVFIY	RGKEYERRED							
DOCK2	FAVGYYG:::GFPSFLRNKVFIY	RGKEYERRED							
DOCK3	FRVGFYGR:::KFPFFL	RNKEYVCRGH							
KIAA0716	FRVGFYGK:::KFPFFL	RNKEFVCRGH							
CLASP-3	FRVGFYGT:::KFGDLD	EQEEFVYKEP							
CONSENSUS	F V FYG	KEY K							
	YF	Q F R							
TRG	PKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD	SKFAYIQVTHVTPFFDEKE							
CLASP-1	PKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLD	PKYAYIQVTVTPFFDEKE							
CLASP-2	PKLTPLSEISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLD	SKYAYIQVTHVTPFFDEKE							
CLASP-4	PKLTGLSEISLRVLVLYGEKFGTENVKIIQDSKDVNAKELDPKYA	HIQVTVKPYFDQKE							
CLASP-3	PAITKLAEISRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAY	IQITYVEPYFDTYE							
KIAA0716	HDYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAQYLQIYAVTPI	PESQE							
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDAILQCDAQYLQIYAVTPI	PDYVD							
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGQY	IQCFVQPVLD							
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGQY	IQCFVQPVLD							
CONSENSUS	L L Y	VIQ+ V P D							
	M F	L E							
CLASP-1	RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN								
TRG	RTILTAIHCFPYVKKRIQVIMYQHHTDLNPIEVAIDEMSKKVAELH								
KIAA1058	RTILTAIHCFPYVKKRIQVIMYQHHTDLNPIEVAIDEMSKKVAELR								
CLASP-2	RTILTAIHCFPYVKKRIQVIMYQHHTDLNPIEVAIDEMSKKVAELR								
CLASP-6	RTILTAIHCFPYVKKRIQVIMYQHHTDLNPIEVAIDEMSKKVAELR								
CLASP-4	RTILTTSNFYPYVKKRIQVIMYQHHTDLNPIEVAIDEMSKKVAELQ								
CLASP-3	KTILTTSHAFPIYKTRVNVTHKEEIIITPIEVAIDEMSKKVAELQ								
CLASP-5	NTVLTTMHAFFPIYKTRISVIQKEEFVLTPIEVAIDEMSKKVAELQ								
KIAA0716	RTSLYLVSPLGISRWFEVEKREVVEMSPLENAIEVLENKKNQQLK								
DOCK2	RTSFVTAYKLPGLRWFEVVMHMSQTTISPLENAIETMSTANEKIL								
DOCK3	RTTLTLTHSLPGISRWFEVERRELVEVSPLENAIQVVENKKNQELR								
DOCK180	RTSFVTAYKLPGLRWFEVVMHMSQTTISPLENAIETMSTANEKIL								
CONSENSUS	RT L FP V + V + P+E AI+ M +L								
	F L L + I								

FIG. 3B (1 of 2)

CLASP-1	SLQLKLQGSVSVKVNAGPMAYARAFLEETNAKKYEDNQV--KILKEIFRQFADACGQALD
TRG	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
KIAA1058	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-2	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-6	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-3	MLQMVLGSGVGTTVNQGPLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR
CLASP-4	QLQLKLQGCVSVQVNAGPLAYARAFLLNDSQASKYPPKKVSELKDMFRKFI--QACSI
CLASP-5	MLQMVLGSGVGTATVNQGPLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFFVKEYILSHPEDGEKIARLRELMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAFFDKDYINKHPGDAEKITQLKELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVRDHPDAHEKIEKIKDLIAWQIPFLAEGIR
CONSENSUS	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="border: 1px solid black; padding: 2px;">L M L+G V VN G</div> <div style="border: 1px solid black; padding: 2px;">Y AFL + + P</div> <div style="border: 1px solid black; padding: 2px;">L+</div> <div style="border: 1px solid black; padding: 2px;">L</div> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-top: 2px;"> <div style="border: 1px solid black; padding: 2px;">L I</div> <div style="border: 1px solid black; padding: 2px;">V V F +</div> <div style="border: 1px solid black; padding: 2px;">I</div> </div>

DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

ref 1.1 ↓

1 31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

↓ ref 2.1

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

FIG. 4A (1 of 7)

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961 991
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
↓ ref 3.1

1081 1111
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501 1531
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561 1591
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621 1651
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

FIG. 4A (2 of 7)

1681
 TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1711
 1741
 AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
 ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1771
 1801
 TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
 ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1831
 1861
 CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
 leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1891
 1921
 GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
 val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1951
 1981
 ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
 thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2011
 2041
 TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
 phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2071
 2101
 GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
 glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2131
 2161
 GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
 ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2191
 2221
 GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
 val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2251
 2281
 TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
 tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2311
 2341
 CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
 arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2371
 2401
 GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
 glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2431
 2461
 AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
 arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

2491

FIG. 4A (3 of 7)

2521 2551
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2581 2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

2761 2791
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2821 2851
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881 2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941 2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH

↓ ref 5.1
3001 3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061 3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121 3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181 3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241 3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301 3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361 3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421 3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

FIG. 4A (4 of 7)

3481	3511
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG	ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA
3541	3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT	TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA
3601	3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC	ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG
3661	3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT	CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG
3721	3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG	TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA
3781	3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT	GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT
3841	3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT	TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT
3901	3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG	AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT
3961	3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA	AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA
4021	
AAC TCG	

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTTCATTTAACTAGCTCAGTTTAATCATGTATTTCCCTATAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAACTCATAGAA
AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT
NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCCTAAGAGCTT
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTTCGTGTTCTGTCNGCAAGNAG
TGCCTATGAAA

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAAGTGTCTCTTAAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTTCATGCTGCTAA
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGAGA
AGGAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACCTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGGAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTCTTTTTGGCAANGTAACTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAACCCCNAAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNNCCCCNATTTATTNATTTATTTATTTTGGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNGGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCCC
TCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG
AGCTCAACNAGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNACCACTTANGAAGCACCACCTGGGGACCTGGAAGGAGANAGANGGNA
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGGNA
TTCTTANNNTAGAGANGAGANAACCTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA. Exon sequence is underlined and represents nucleotides 3000-3492.
This region does not contain a intron in this region

CCANNAGATTNNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNNTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCTTCTTNCAAGGGTTNCTAGGGCC

FIG. 4A (7 of 7)

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGPVFTRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLHLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLHLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 4B (1 of 5)

HC2A IIHVVAQCHEEGLESHLSRVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
 KIAA IIHVVAQCHEEGLESHLSRVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
 rat -----
 HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
 HC1 LPDIVAKCHEEQLDHSVQSYIKFVKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
 HC3 TQAMDRSCNRMSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
 HC5 -----

Cadherin
 Cleavage

HC2A KLLRYSWFFFVDLIKMAQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGD
 KIAA KLLKYSWFFFVDLIKMAQHLIENSKVKLLRNQRFPPASYHHAVETVVNMLMPHITQKFRD
 rat -----
 HC4 KLLKYSWFFFETIAKSMATYILLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
 HC1 HVLKHSWFFFATILKMAQHLIDTNKIQLRPQRFPPESYQNELDNLMVLSHDHVIWKYKD
 HC3 SALQQAWFFFELMVKSMVHHLYFNDKLEAPKSRFPFERFMDIAALVSTIASDIVSRFQK
 HC5 -----

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDHKTLEFYKFEFL
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
 rat -----
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
 HC1 ALEETRATHSARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
 HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVIVSLRLDFL
 HC5 -----

HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
 KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
 rat -----
 HC4 QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL---EYSLSDEY
 HC1 QEVCQHEHFIPCLPIRSANIPDLTPSES-----TQELHASDMPESYVTNEF
 HC3 RIICSHHEHYVTNLPCSLTTPASPSVSSATISQSSGFSTNVQDKIANMFELS--VPF
 HC5 -----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVP

1.1

Cadherin
 EC motif

HC2A CRNHFLVGILLREVGTALEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
 KIAA CRNHFLVGILLREVGTALEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
 rat -----
 HC4 CKHHFLVGILLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
 HC1 CRKHFLIGILLREVGTALEQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
 HC3 RQQHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDFQIKARVAM
 HC5 SSTS-SPGILFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCVPEVKVIAA

HC2A LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
 KIAA LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
 rat -----
 HC4 LYLPLFVGLLLENIQRLAGRTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
 HC1 LYMPLYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
 HC3 LYLPLIGIIMETVPQLYDFTETHNQRGPICIATDDYESE-----SG---SMIS
 HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

FIG. 4B (2 of 5)

		Refs
HC2A	KDLLGAISGIA I SPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
KIAA	KDLLGAISGIA I SPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGIIKREDSRGSLLIP-EGATGFPDQNGTGEN-----TRQS	
HC1	KDVLNSIA I AFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	
HC3	QTVAMAIAGTSVPQ-----LTPGFSFLLTSTSGRQHT-----	2.1
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLFPYKQYN-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDLLTYWN-KVSPQELINILILEVCL	
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIPVCL	
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLCV	
HC5	-----MLNADTTNRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	
KIAA	HQFQYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGKRNIARVHDAWLKSHFGIDRKS-----QTMPALNRNRSGVM	
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGTGKSNPSCQTSGLLAQWMHSTSRHEGK	
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSTTTEADIFHQALLEGNTATEVS	
HC1	QHRSQLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHVDTEANIATEGC	
HC3	RRSRGQILERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN	
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFK I NQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
KIAA	LTALDTLSLFTLAFK I NQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMAKNVFTALRSLIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC	
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLQHC FATQRALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRAIA	3.1
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH	
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH	
HC3	KFPPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK	
HC5	KFGDLLFEEVEQCQFDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK	
HC2A	LQVIIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVIIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVIIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFA NSDRPMLARAFPAEVKDLTKRIRTVLM	
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNNBNFPAEVKDLTKRIRTVLM	
HC3	MQVPMSSLSLVGTSQNFNEEFLRRSLKTI LTYAEDLELRETTFPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILY	

FIG. 4B (3 of 5)

Transmembrane

Refs

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKN	DLSEAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE SMAKIHARNG	DLSEAMCYIHI
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTSPDLRLTWLQNMAGKHSERS	NHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQASPDRLRLTWLQNMAEKHTKKK	CYTEAAMCLVHA

SH3

HC2A	TALVAEYL	TRKGV-----	-----FRQGCTAFRVITPN
KIAA	TALVAEYL	TRKEA-----	-----VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYL	TRKEAD-----	-----LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFL	HRKKL-----	-----FPNGCSAFKKITPN
HC1	AALIAEYL	KRKG YWKVEKICTASLLSE	THPCDSNSLLTTPSGGSMFSGMGPFLSITPN
HC3	AALVAEYL	SMLD-----	-----RKYLPVGCVTFFQNISSN
HC5	AALVAEYL	SMLD-----	-----HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLELLEQCVNGLWKAERYEII	SEISKLIGPI
HC1	IKKEGAAKEDSGMHD-----	TPYNEINILVEQLYMCGEFLWKSERYELIADVNKPI	IAV
HC3	VLEESAVSDDVVSPEDEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVL	IPI
HC5	VLEESVVSSEDTLSPDEGDVCGAQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKVL	IPI

		ITAM	ITAM		ITAM	ITAM
HC2A	YEKRRD-----					
KIAA	YEKRRD	FERLAHLYDTTHRAYSKVTEVMHSGRRL	LGTYFR	VAFFGQAAQYQFTD	SETDVE	
rat	SMKSGGTLETTHLYDTTHRPYSKVTEVITR-----			A-----	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRL	LG-----			TFRRVAFYQG	
HC1	FEKQRDFKKLSLYDYDIHRSYLVKVAE VVNSEKRL	FG-----			RYRVAFYQG	
HC3	HEANRDAKKLSTIHGKLQEA FSKIVHQTGWERM	FG-----			TYFRVGFYG-	
HC5	LEAHREFRKLTLTHSKLQRAFD SIVNKDH--	KRMFG-----			TYFRVGFYG-	

		ITAM		ITAM
HC2A	-FFEDEDGKEYIYKEPKLTP	PLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKEYIYKEPKLTP	PLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTP	PLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEEDGKEYIYKEPKLT	GLSEISLRLVKLYGEKFGTENVKIIQDSKVNPAKELDPKYA		
HC1	GFFEEEDGKEYIYKEPKLT	GLSEISQRL	KLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRIE	QFYGERFGEDVVEVIKDSNPVDCKCLDPNKA		
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFY	GCQCFGAEFVEVIKdstpVDKTKCLDPNKA		

4.1

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVYKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRTILT
HC1	YIQVTVYVTPFFEEKEIEDRKTD FEMHNNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFQRKRTILT
HC5	YIQITYVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

FIG. 4B (4 of 5)

	Coiled-Coil 1
HC2A	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSSTDVDMIQQLKLQGSV
HC1	SHLFFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFFPYIKTRVNVTHKEEIIILTRIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV
HC5	MHAFFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPDAKMLQMVLOGSV

	Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLNDSQASKYPKKVSELKDMFRKFIQACSTALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

	Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVMHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	YQEEMKANYREIRKELSDIIVHICPGEDKRATKFFPAHLQRHQRTDNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASISGTSDDRGYGSPPRYA
HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDLK---RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG----KLSS-----P-----
HC5	YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPHEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMNGGREKEPWTVIFNSRFYRSWCK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----
RNTVLT	

FIG. 4B (5 of 5)

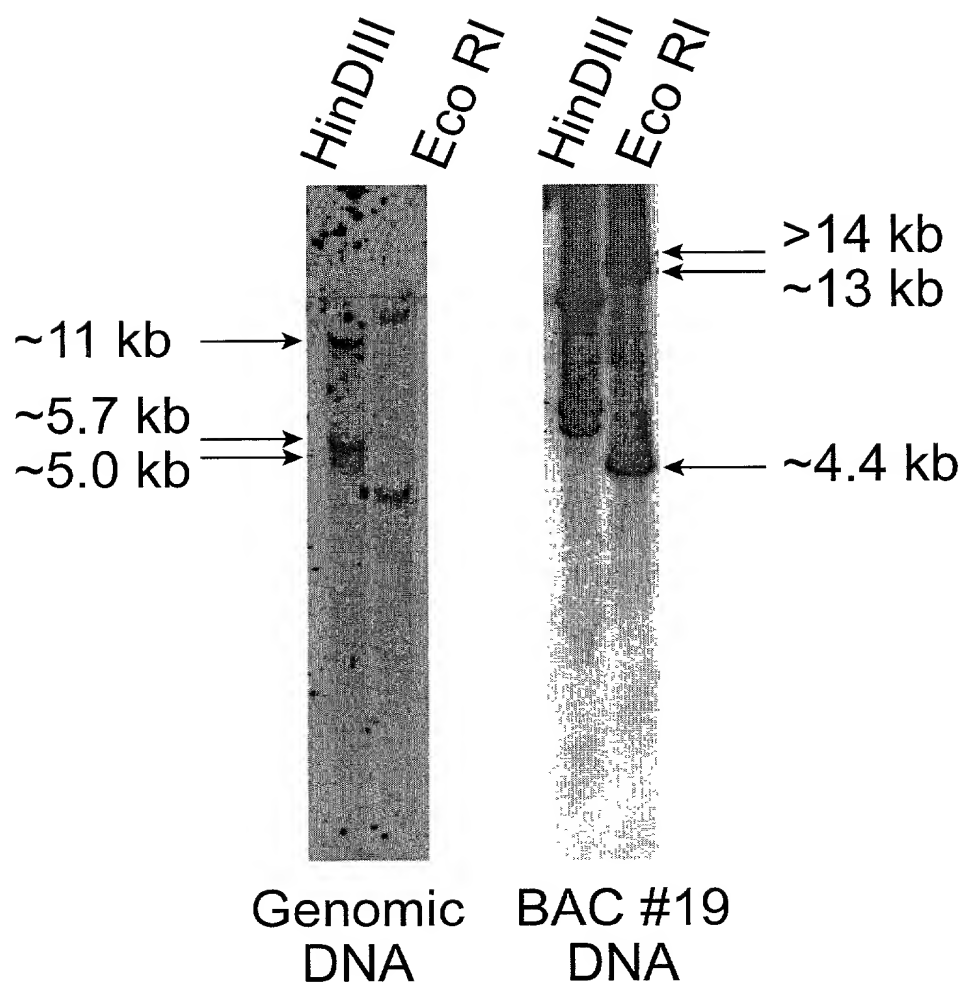


FIG. 5

-111

CGGTAACCGCCATTTTGTCTCCTGTAAACAATTTACGCGCCGTGTAAGTGTGAATCTTTCAAAGCCTCAGTTTATGACC
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1	31/11
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG	CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT
Met thr his leu asn ser leu asp val gln	leu ala gln glu leu gly asp phe thr asp
61/21	91/31
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG	GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG
asp asp leu asp val val phe thr pro lys	glu cys arg thr leu gln pro ser leu pro
121/41	151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC	AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val	arg asp cys val gln thr tyr ile arg glu
181/61	211/71
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA	AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly	ser pro glu ile cys gly phe lys lys thr
241/81	271/91
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT	CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu	pro lys gln thr phe glu ser glu thr leu
301/101	331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC	CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly	pro arg his leu asn val leu cys asp val
361/121	391/131
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC	TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG
ser gly lys gly pro val thr ala cys asp	phe asp leu arg ser leu gln pro asp lys
421/141	451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT	GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser	ala glu asp phe glu lys gln asn glu glu
481/161	511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC	TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu	phe ala leu tyr pro ser val asp glu glu
541/181	571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA	TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu	cys pro lys glu his leu gly asn arg ile
601/201	631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG	ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT
leu val lys leu leu thr leu lys phe glu	ile glu ile glu pro leu phe ala ser ile
661/221	691/231
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG	ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys	ile ser glu asn phe his cys asp leu asn
721/241	751/251
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT	CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG
ser asp gln phe lys gly phe leu arg ala	his thr pro ser val ala ala ser ser gln
781/261	811/271
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC	CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG
ala arg ser ala val phe ser val thr tyr	pro ser ser asp ile tyr leu val val lys
841/281	871/291
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT	GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile	gly asp cys ala glu pro tyr thr val ile
901/301	931/311
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA	AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA
lys glu ser asp gly gly lys ser lys glu	lys ile glu lys leu lys leu gln ala glu
961/321	991/331
TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG	ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA
ser phe cys gln arg leu gly lys tyr arg	met pro phe ala trp ala pro ile ser leu

FIG. 6A (1 of 6)

1021/341	TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG	1051/351	AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
ser ser phe phe asn val ser thr leu glu		arg glu val thr asp val asp ser val val	
1081/361	GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA	1111/371	TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
gly arg ser pro val gly glu arg arg thr		leu ala gln ser arg arg leu ser glu arg	
1141/381	GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA	1171/391	TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
ala leu ser leu glu glu asn gly val gly		ser asn phe lys thr ser thr leu ser val	
1201/401	AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC	1231/411	CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
ser ser phe phe lys gln glu gly asp arg		leu ser asp glu asp leu phe lys phe leu	
1261/421	GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG	1291/431	AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
ala asp tyr lys arg ser ser ser leu gln		arg arg val lys ser ile pro gly leu leu	
1321/441	AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC	1351/451	ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
arg leu glu ile ser thr ala pro glu ile		ile asn cys cys leu thr pro glu met leu	
1381/461	CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA	1411/471	CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA
pro val lys pro phe pro glu asn arg thr		arg pro his lys glu ile leu glu phe pro	
1441/481	ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG	1471/491	TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
thr arg glu val tyr val pro his thr val		tyr arg asn leu leu tyr val tyr pro gln	
1501/501	AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA	1531/511	GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
arg leu asn phe val asn lys leu ala ser		ala arg asn ile thr ile lys ile gln phe	
1561/521	ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG	1591/531	CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
met cys gly glu asp ala ser asn ala met		pro val ile phe gly lys ser ser gly pro	
1621/541	GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT	1651/551	ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
glu phe leu gln glu val tyr thr ala val		thr tyr his asn lys ser pro asp phe tyr	
1681/561	GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG	1711/571	CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
glu glu val lys ile lys leu pro ala lys		leu thr val asn his his leu leu phe thr	
1741/581	TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA	1771/591	GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
phe tyr his ile ser cys gln gln lys gln		gly ala ser val glu thr leu leu gly tyr	
1801/601	TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT	1831/611	CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
ser trp leu pro ile leu leu asn glu arg		leu gln thr gly ser tyr cys leu pro val	
1861/621	GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC	1891/631	ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
ala leu glu lys leu pro pro asn tyr ser		met his ser ala glu lys val pro leu gln	
1921/641	AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT	1951/651	AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
asn pro pro ile lys trp ala glu gly his		lys gly val phe asn ile glu val gln ala	
1981/661	GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC	2011/671	CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
val ser ser val his thr gln asp asn his		leu glu lys phe phe thr leu cys his ser	
2041/681	CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC	2071/691	GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
leu glu ser gln val thr phe pro ile arg		val leu asp gln lys ile ser glu met ala	
2101/701	CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC	2131/711	TGC CTG AAC TCC TCC CGC CTG GAG CCG CTC
leu glu his glu leu lys leu ser ile ile		cys leu asn ser ser arg leu glu pro leu	

FIG. 6A (2 of 6)

2161/721	2191/731
GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG	CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
val leu phe leu his leu val leu asp lys	leu phe gln leu ser val gln pro met val
2221/741	2251/751
ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG	TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
ile ala gly gln thr ala asn phe ser gln	phe ala phe glu ser val val ala ile ala
2281/761	2311/771
AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC	AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
asn ser leu his asn ser lys asp leu ser	lys asp gln his gly arg asn cys leu leu
2341/781	2371/791
GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG	CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
ala ser tyr val his tyr val phe arg leu	pro glu val gln arg asp val pro lys ser
2401/801	2431/811
GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG	AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
gly ala pro thr ala leu leu asp pro arg	ser tyr his thr tyr gly arg thr ser ala
2461/821	2491/831
GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC	CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
ala ala val ser ser lys leu leu gln ala	arg val met ser ser ser asn pro asp leu
2521/841	2551/851
GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA	GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
ala gly thr his ser ala ala asp glu glu	val lys asn ile met ser ser lys ile ala
2581/861	2611/871
GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT	TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
asp arg asn cys ser arg met ser tyr tyr	cys ser gly ser ser asp ala pro ser ser
2641/881	2671/891
CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG	CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
pro ala ala pro arg pro ala ser lys lys	his phe his glu glu leu ala leu gln met
2701/901	2731/911
GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG	GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
val val ser thr gly met val lys ser met	ala gln his val his asn met asp lys arg
2761/921	2791/931
GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC	CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
asp ser phe arg arg thr arg phe ser asp	arg phe met asp asp ile thr thr ile val
2821/941	2851/951
AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT	TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
asn val val thr ser glu ile ala ala leu	leu val lys pro gln lys glu asn glu gln
2881/961	2911/971
GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC	TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
ala glu lys met asn ile ser leu ala phe	phe leu tyr asp leu leu ser leu met asp
2941/981	2971/991
CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT	TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
arg gly phe val phe asn leu ile arg his	tyr cys ser gln leu ser ala lys leu ser
3001/1001	3031/1011
AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA	GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
asn leu pro thr leu ile ser met arg leu	glu phe leu arg ile leu cys ser his glu
3061/1021	3091/1031
CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG	AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
his tyr leu asn leu asn leu phe phe met	asn ala asp thr ala pro thr ser pro cys
3121/1041	3151/1051
CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC	TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
pro ser ile ser ser gln asn ser ser ser	cys ser ser phe gln asp gln lys ile ala
3181/1061	3211/1071
AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC	CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
ser met phe asp leu thr ser glu tyr arg	gln gln his phe leu thr gly leu leu phe
3241/1081	3271/1091
ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA	GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA
thr glu leu ala ala ala leu asp ala glu	gly glu gly ile ser lys val gln arg lys

FIG. 6A (3 of 6)

3301/1101	GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT	3331/1111	TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
3361/1121	ala val ser ala ile his ser leu leu ser	3391/1131	ser his asp leu asp pro arg cys val lys
3421/1141	CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT	3451/1151	TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
3481/1161	pro glu val lys val lys ile ala ala leu	3511/1171	tyr leu pro leu val gly ile ile leu asp
3541/1181	GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT	3571/1191	GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
3601/1201	ala leu pro gln leu cys asp phe thr val	3631/1211	ala asp thr arg arg tyr arg thr ser gly
3661/1221	TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC	3691/1231	ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
3721/1241	ser asp glu glu gln glu gly ala gly ala	3751/1251	ile asn gln asn val ala leu ala ile ala
3781/1261	GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA	3811/1271	ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
3841/1281	gly asn asn phe asn leu lys thr ser gly	3871/1291	ile val leu ser ser leu pro tyr lys gln
3901/1301	TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC	3931/1311	AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
3961/1321	tyr asn met leu asn ala asp thr thr arg	3991/1331	asn leu met ile cys phe leu trp ile met
4021/1341	AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG	4051/1351	TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
4081/1361	lys asn ala asp gln ser leu ile arg lys	4111/1371	trp ile ala asp leu pro ser thr gln leu
4141/1381	AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT	4171/1391	GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
4201/1401	asn arg ile leu asp leu leu phe ile cys	4231/1411	val leu cys phe glu tyr lys gly lys gln
4261/1421	AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG	4291/1431	CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
4321/1441	ser ser asp lys val ser thr gln val leu	4351/1451	gln lys ser arg asp val lys ala arg leu
4381/1461	GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC	4411/1471	AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
	glu glu ala leu leu arg gly glu gly ala		arg gly glu met met arg arg arg ala pro
	GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA		AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
	gly asn asp arg phe pro gly leu asn glu		asn leu arg trp lys lys glu gln thr his
	TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA		ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
	trp arg gln ala asn glu lys leu asp lys		thr lys ala glu leu asp gln glu ala leu
	ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT		TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
	ile ser gly asn leu ala thr glu ala his		leu ile ile leu asp met gln glu asn ile
	ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA		GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
	ile gln ala ser ser ala leu asp cys lys		asp ser leu leu gly gly val leu arg val
	CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT		ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
	leu val asn ser leu asn cys asp gln ser		thr thr tyr leu thr his cys phe ala thr
	CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC		TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
	leu arg ala leu ile ala lys phe gly asp		leu leu phe glu glu glu val glu gln cys
	TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC		TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
	phe asp leu cys his gln val leu his his		cys ser ser ser met asp val thr arg ser
	CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG		AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
	gln ala cys ala thr leu tyr leu leu met		arg phe ser phe gly ala thr ser asn phe
	GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC		CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC
	ala arg val lys met gln val thr met ser		leu ala ser leu val gly arg ala pro asp

FIG. 6A (4 of 6)

4441/1481	4471/1491
TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG	AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
phe asn glu glu his leu arg arg ser leu	arg thr ile leu ala tyr ser glu glu asp
4501/1501	4531/1511
ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC	CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
thr ala met gln met thr pro phe pro thr	gln val glu glu leu leu cys asn leu asn
4561/1521	4591/1531
AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG	GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
ser ile leu tyr asp thr val lys met arg	glu phe gln glu asp pro glu met leu met
4621/1541	4651/1551
GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC	CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
asp leu met tyr arg ile ala lys ser tyr	gln ala ser pro asp leu arg leu thr trp
4681/1561	4711/1571
CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG	AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
leu gln asn met ala glu lys his thr lys	lys lys cys tyr thr glu ala ala met cys
4741/1581	4771/1591
CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG	TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
leu val his ala ala ala leu val ala glu	tyr leu ser met leu glu asp his ser tyr
4801/1601	4831/1611
CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT	ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
leu pro val gly ser val ser phe gln asn	ile ser ser asn val leu glu glu ser val
4861/1621	4891/1631
GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG	GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
val ser glu asp thr leu ser pro asp glu	asp gly val cys ala gly gln tyr phe thr
4921/1641	4951/1651
GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG	GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
glu ser gly leu val gly leu leu glu gln	ala ala glu leu phe ser thr gly gly leu
4981/1661	5011/1671
TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG	GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
tyr glu thr val asn glu val tyr lys leu	val ile pro ile leu glu ala his arg glu
5041/1681	5071/1691
TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG	CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
phe arg lys leu thr leu thr his ser lys	leu gln arg ala phe asp ser ile val asn
5101/1701	5131/1711
AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC	TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
lys asp his lys arg met phe gly thr tyr	phe arg val gly phe phe gly ser lys phe
5161/1721	5191/1731
GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC	AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
gly asp leu asp glu gln glu phe val tyr	lys glu pro ala ile thr lys leu pro glu
5221/1741	5251/1751
ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT	CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
ile ser his arg leu glu ala phe tyr gly	gln cys phe gly ala glu phe val glu val
5281/1761	5311/1771
ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC	AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
ile lys asp ser thr pro val asp lys thr	lys leu asp pro asn lys ala tyr ile gln
5341/1781	5371/1791
ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG	TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT
ile thr phe val glu pro tyr phe asp glu	tyr glu met lys asp arg val thr tyr phe
5401/1801	5431/1811
GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG	TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
glu lys asn phe asn leu arg arg phe met	tyr thr thr pro phe thr leu glu gly arg
5461/1821	5491/1831
CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA	AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
pro arg gly glu leu his glu gln tyr arg	arg asn thr val leu thr thr met his ala
5521/1841	5551/1851
TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC	ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG
phe pro tyr ile lys thr arg ile ser val	ile gln lys glu glu phe val leu thr pro

FIG. 6A (5 of 6)

5581/1861 5611/1871
ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn
5641/1881 5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr
5701/1901 5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro
5761/1921 5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys
5821/1941 5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln
5881/1961 5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys
5941/1981 5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his
6001/2001 6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTCCACAATGTACCAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCTCTGCCCCATATTTGAATTTATGGAGTAACCTCAAATTCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCAAAAATCATCATGTTGGAAATTTGGGAGGAGATTATTTGTGAACCTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTATAAAGCAATAATATCTCTGTTTTTCATTTTCAAGACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAATTTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAA
AAAAAAAAAAAACTCG

FIG. 6A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

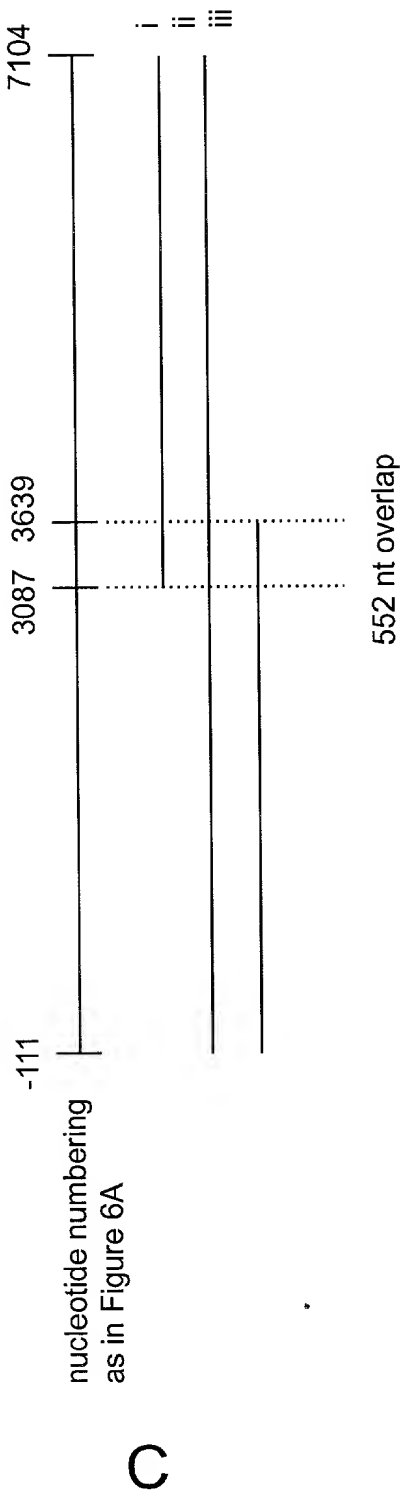
B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

FIG. 6C



1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)

GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAACCTCTTGATTCCCTGTGTTGTGCCAACAGAAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTTTCATTGCAGTTGCAGATACTCGCA
GATACCGCACCAAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACAACTTTATAACCAGC

6th exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCCGG
CTGGAAGAGGCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGAGATGATGCGC
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCCTGCTCTCTGTCAAGC

FIG. 7A (1 of 4)

7th exon (nucleotides 20928 to 21015)
TCAAATTCCTATCATGCATTTCTTAACTCCTAGGGAACGACCGATTTCCAGGC
CTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)
GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTG

9th exon (nucleotides 27242 to 27376)
GGATTCAATGATGCTGTTCTTCCATTCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)
AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC
CTCATGAGGTTCAAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)
TTACTTCATCTTTTTTTTTTTTTTTTCACTGATGCAGAAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCTTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)
AGCTAAGATTATTTTGGAGGCTTACACTTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTTTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATT

13th exon (nucleotides 33663 to 33855)
TCCTCAAACTACTTCTCACTCAATCTGTCTTCAGAATTGCCAAGAGTTACCA
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACACAC
CAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGT
GGGCAGTGTGAGCTTCCAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTG
GTT

FIG. 7A (2 of 4)

14th exon (nucleotides 38125 to 38268)

CTGTTCTCCAGGCTTATACTGTGGTCTCTTTTCAGAAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTGTG
CGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)

AATTCTCTCTGATGCTCTTCTCCTCTTTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTTTATATTTTGGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACCAAGGTATACAAAAATTTACAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)

TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGA
ATTTCAACCTCCGGAGGTTTCATGTACACCACCCCGTTACCCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGCACGCCTTCCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)

ACAGTGA CTTCCTATGTTTACGTCTCATGTT CAGTTTGT TTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCTGT
GGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

20th exon (nucleotides 50892 to 50998)

TATATTCTTTTTTTTTTTTTTTTTTTTTTTTCCCACCAGGGACCACTGGAAGTAGC
CCAAGTGTTTTTGGCTGAAATTCCTGCTGATCCAAACTCTATCGACATCACAACA
AGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG
GCTGGGAATTT CAGTAGAG

FIG. 7A (3 of 4)

21st exon (nucleotides 62398 to 62568)
TCATTTATTTCTCCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC
TCAAAAAGAAGCTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)
CCTCCCTCTCTTTTCTTAATTTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTTCACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTTCT
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACCTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
ATTTGTGAACCTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
TTTTGTTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC
TTTTTTTCTTATGTCACCTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCA
GTTTCTTTTTTATAAAGCAATAATATCTCTGTTTTTCATTTCAGAACATTGTGCTG
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT
ATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAA

FIG. 7A (4 of 4)

AGAGCATCAGGCAAAATTTCTCATTATTAGGTTATATTTCTGTTGCATATTCCTTGATACTAGTACAAAAGTGAAGGCTT
 GTCTTACTAATTGAAAAAAATCTTAGCCATATATGCCATATGGCATGATCCAGATATTAGCTACATGACCATCTTACT
 GTGAACAGGGAAAGATCTGACTCACAAGCAGCAATTCAAAATGTATAAACTTTTTGCTCCATCCTGCCAGCAGCTTAAG
 TCCTAAAATTCCTTGGACTAAGCTTACCTTAGGTTCTTTCCACCTTCCCTTCTGACTGCCCCAGGGAGTGCCCAAC
 CCAGGGGCCAGGCTCACAAAACCATGAAGGATTTCTAAAGACACTTTAGATGCTCTTAATGAAATATAAAGTGTGCTCCC
 AGGATACAAATACAGGACAGGAATTACTGAGGACCGGTAATCTAATACTTCCCTCCCTGACATCACTTGTAGTTCCAGG
 CCAGCAAAAGTCTGACAATGTGCTTAAGCCAAATTCAGAAGTGTAGCTGAGGCCGGGCACGGTGGCTCACATTTGTAATC
 CCAGCATCTTCGGAGGCCAAAGGGAGTGGAATACTTGAGGCAGGAGTTACCAGCCTGACCAACATGATGAAAACATCATAT
 CTACTAAAAATACAAAATGCATCAGGTGTGGTAGTGTGACTGTAATCCCAGCTACTTGGGACGCTGAGGCATGAGAATT
 GCTTGAACCCGGGAGAGGGAGGTTGCAGTGAGCTGAGACCATGCCACTGCAATCCAGCCTGGGTAACAGAGTGACACTCT
 GTCTTTCAAAAAAAGGAGGATTTGAGTACCTGAGTAAGCAGGGCCTTAAACAAAGGGGCGCATTTGGTTACAG
 AGGAATTGCCTGTTCCAGCCCCAGGACTGGGTGAGGTTCTTATTTCTGTGCAACTTTTATGCTAGGATTTTTATCTT
 CAGCTTTTGATTTTCAAGGTGGGAAAGGGAGCGTCATTCATTTTCAACAGACCCGGGGTGCTTTATTTTCATCTTTCCCGC
 TGGGAGTCTTCTCTGTGGGTATGGGAAAGTGCAGTAACCACTCTGTGCCTCAGTTTCCCTGTCCGCTTATCTGGCA
 CCAGAGTACCTACCTCACTGGGAGGGCTCACGAAGCCTGGCTGGGGCGAGGACTCAGTAAACACTGGCCATCGCTATTT
 TCATTCCAGTTCTTGTGGCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGTCTGCTCCAGCTTCCAGGACCA
 GAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCAGCAGCACTTCTCACCAGGCTCCTTTCACAGAACTGG
 CTGCTGCCCTGGATGCCGAAGGGGAAGGGTATGTTTCTGGCATTATAAATGGAAGATGAAGCAAAAAAAGAGATGTTCT
 TTAATAAAATTTGCAGTCTAGCTTCTCACACTTGGTAAAAAATCTACTGTAGTTGACCACTTCTGAGGAGTAGAAACAT
 CTGCTTGTAGAATATGGTACCCATAAGCACAGGCACAAAGAGGCTTCTTGTGTAGAAAGGCACAGGGATGGGTAA
 GAACTACAAAATGACTTTTCTTGGTCAACTATTTTCAAGTGAATTTACCAGTTCTGCTATAGCAGGTTTCCCAAGGATGCT
 TTGATTAGTGAACCTCCCTAGGAGCAAAGCCATTTTAAACAAAGGGGATAGCATGCAGAGGCAACCACAAGATGTCACCTG
 GTTCAAAGCTGATGAAGGAAATTAATGGCTGCTGAGAAGGCAGCTGTCCCATGCCAGATTAGGTTTCTTGCAGACAGTGC
 TTCTCAGGCCAAGAGACACCACACATCCAGGGCTTCTGAATCCTTTTACCTCTTATCTATCTGATTACTCAGGGACATGT
 GGCAGTATCTAGCCTAGAAGTCAACAGACAGAGAGGTAGACCACCCCTTCTTTCCCTCTCTCCCTATGCTCCGTGAGCT
 CATGGAGTCAGAAACCCACAGCCTATCTGATTGGACTGAAAAGATAATGCCCTTCTAAAATATTATTTCATTCCTGTAAC
 AATTATTGAATGCCCTCCATGGGACAGACACAGTTAGGTGTTAGAGTACATCAGAGATATATCAGTGCACAAAACAGACA
 AAATTCGCTGCCCTCAAGAGCTCACCATCCAGGGACTCAGATTCAGAGATGATTAGGATTGCAAGTAGTTGAGATTCA
 ACATTTCTGGTGTATTAGATTAGGCATACAGAAATGACAGGAACTTGCCCACTATTCCATAACAGAGAAAGCAATCTAAAGC
 CATGGTCTTCCAGTCCCTTCCAGGACCCACTCTCTATACCAAAACCATCTCCCTGCACAGGGAACCTGTTCCCATGAC
 TCCTATGCTAAAGAGGTTTCCAGAATAATGTTTGCTAATTAATGGTAGCATTGCTGTATGTTATGGATGGATTTTTATCT
 AAATGGAATTTCTCAAGTTCTCTCAAGTGCTTACAATTTAGTGAAGGAAACAGGAGGTTTCCCTGCATGAAACAAATACAG
 GAGCACATCGAGTTCTGTGCAACTGCAACAGTCACATGTGTCCTCAAGCTATGTACCCAGGCTGACACCGCTGAAGTGACTC
 TATGCTGCGTCTCCTGGCAGGATAGTGTGGGAATCTCATGCTTTAGCTCTCAATTTGCTCCTTCCAGATAAAGTGA
 GCCTGAGTATATCTTTGAGAATCTTCACTTTCCATGGCTTCAATTCTATCTTCTCTCAACTCTAACTAAATTTCTCC
 CAATTATCTCAGTAGAATGTTCTACCTACAATAACATAAATTTCCACAGCAACAAAAAGTGCACCGAACACTTATGCT
 AATAAGTAAGATACGAGAAGAAAGTTTGAACACAAAGAAATTGCTTCATGCACAAACATGTACATACATTTTCTTAG
 TTGTCCTTTAATAGCAGTACTTTAAGTGATTTCTAGAAACATCTTTAGTATTTACAATAGCGTAGTTTCTATTTTCTATT
 TTCATTCTAGCTGGAAACAGCCATGACATTTCTGTTCTGGATTCTTGTAAAATTTGTTGCTGTTATATTACTAGCAACAAG
 GTAGAGTATATTACAGAGATAATCATGTAATTATGTTTAATCAGGTAGATACATTCTTCAAACACACACACACACACAC
 ACACACGCACACACCGCGGTGCACATGCACACACACAGTACCCTTTCTCCCCAAAAGAGTAATTAACAGTGTAACCTCT
 TTGGCAACACAGTAATCCCTGATTGCTGGGTTGTGAGTTACTCTCTGGAAGTCAATTAGATACACTGTCACAACCTCAT
 CATGTAAGCTAAACCTCAGAAAAATGTCATGCTTCAACAATACTTCCCTATTGATCAGCACTTCTTTTTTTTTTTCTTT
 TGCTTCCAAGACAGTTGGTAGACTTGCCAACACCTGTACATCCATGGGGCAAGGGCCAGAAGGACGCATCTCAGTACCTG
 AACCCCTAGGGAGCTACAGCTCCAGTTTCCACTGGGTTTCCCTTGGATCTCTGACACCTGGGTATATCCCAAGTGTCTA
 TGCATCGTTAAATCCACAGTGTTTTTCAAGCATTTAGAAATTTGTCTATCATCTTTGTGTTAAGCCAGCAAAATGCAATGC
 CTAATTCAAAACACAACCCATTGCCGGGACCACAGACTAAGAACAAGAAAACTTTTGAATGCAATTTACAATTATCTT
 ACTTTAGCCACAGTGAAGAGTCTGAGTCATTTAAAATTTTGGTTAATATTTTCTATATAACGTTGAATTTCTGATGTAGC
 CTTATTTTGTGTTGAAGAAAAAATGTATATATATGTATATATTTTTTAAATCTGGATTCTTTTTTTTATTATTATCATAC
 TTTAAGTTCTAGGGTACATGTATACAACATGCAGGTTTGTACATATGTATATATGCGCCATGTTGGTGTGCTGCACCCA
 TTAACCTCGTCACTTACATTAGGTATATCTCCTAATGCTGCTGCCCTCCCCACTCCCCCACCCTACGACATCCCCGGTGTG
 TGATGTTCCACCTATGAGTGAGAACATGCGGTGTTTGGTTTCTGTCTCTGCGATAGTTTGTGAGAAATGACGGTTTTT
 AGCTTTCATCCATGTCCCTACAAAGGACATGAACCTCATCTTTTTTATGGCTGCATAGTATCCATGGTGTATATGTGCCA
 CATTTTCTTAATCCAGTCTACCATTTGATGGACATTTGGGTTGGTTCCAAGTCTTTGCTATTGTGAATAGTGCCGCAATAA
 AAGGATTATAAATCATGCTGCTATAAAGACATATGCACACATATGTTTATTGCGGCAAGATGTATATTTTAAATTTGAA
 CATCTATGACTAGGTTCCAGATACTCCACTATATATTTTATTACTTTTTATTATAGTATAATTTATATAAAGAACCTGA
 ATCCTAAGTGTAAGTGCAGTTAATATTTCTGTGAATATATTTGAGTAACCACAGTCAGATAAAAAATATAATATTC

FIG. 7B (2 of 15)

CATTATCCTCTCTCAGTTACAGGCCCCCTCAAGTAACCACTATTCTGACTCTTATTATTAGAAATTAATACTGCCTGTT
 GTTGAATTTTCATAGTCTTTTCTGCTGAATGTTGTGACTGTGACATCCTTTAGTGTGGTGCATGTGTGAGTATTCATTTTTT
 TTCAACTGTATGTCATATTCTTTGTCTACTATAATTTCTCTTCTGTAAATTGACATTTGGGCTGCTTTCTATTTGTGGG
 TATTGGGTATTATGAAAACAGCTGCCGTGAACATGCCTGTGCATGGTTTTGGGTGGACGTTAGAACTCATTCTTTGGGG
 CTATAAATACAGCCTATTTTTTATTTAATATACTGCTCTTGAATAGTTTAATAAATATGTGTACATGGTCTTAACAAA
 TGTCAAAAGAATATACTCTGAGCTAGGAAAAGAAGAGCAAAGTCAAAGCAGGAAGATGGCAGGAATAACAAAGGTG
 ATAGCCAAAATAAATGAAATAAAGAATAGAAAACAATCACGGAAATCCGCAAGATGAAAAGCTTGTATTGTGAAAAGAG
 CAACAAAATTCACCAATCTTTAGCTGAGCTGACCAAGAAAAAGGAAGAAGACTCAATTACTAAAAATCATAATTGAAAGA
 TTCAACACAATCATATCACAAGAGACCTTACAGAAATAAAAAGGATTATAAAGAATACGATGAACAATTGAAAGCCATC
 AAATTGATAACCTAGATTAAATGGATAAATTCCTTAAAAGGTACAAAGTACTAAAATTGACTCCAAGAAGATATAGAAA
 TCCAAATAGACCTACAGAAGTAAAAAGATTGAGTTAGTAATCAAACCTCCACATACACCTACTATGTACCCACACAAAT
 TAAAAATTTAGGCTGGGCGCAGTGGCTCATACTGTAATCCCAGCACTTTGGGTGGCCAAGGCGAGTGGATCACCTGAGG
 TCAAGAGTTTCAAGCAGCCTGGCCAAGGTGATGAAACCCCGTCTCTACTAAAAATACAAAAATTAGTGGGTGTGGTGG
 CGGGAACCTGTAATCCCATCTACTCGGGAGGCTGAGGCAGAAGAATCATTGAGACTGGAAGGCAGAGGTTGCAGTGAGC
 CAAGATCATGCCAATGCACCTCCAGCCTGGGCAACAAGAGCAAACTCCATCACAATAATAATAATAATAATATATT
 TTAAATTTAAACTTCCTACAATAAAAGCTCAAACCTGGGGGGCTTTACTGATGAATTCTACCAATATTTTTAAAGA
 ATTAATTTCTAATTTTTTACCAACTTCCAGTCTTCTCTTCCAACGATGGAAGAGGTGGAATACTTCCCCACTTGTCTAT
 GAAGCTAGCATTACCTATACTAAACCAGACAAAGACATCATGAGAAAACCTACAGGCCAGTATCTGATGAATATAGATGT
 AAGACCTCAACAAACACTAGCAAACCTGAATCCAACAGCATATAAAAAGGATTATACACCATGGCTAAGTAGGATTTATC
 TCAGGAATGCAAGATAGGCTGCATACCTGAAAATCAATTGTTGTACCATATTAATAAAATAAAGGACAAAACCCATACAA
 TCATCTTAGTAGATGCAAGAAAAGCATTTAATAAAATCTAATAACGCTTCTTGATAAAAAACACTCAACAAACCTTTTAG
 GAAATAAGAGAACTTCCTCAACTTGACTTAAGGGCCTCTATGAAAAATCCACAGCTAATGTGACACTTATTAGTGAAAA
 CAGTGTCTTATCCCTAAGATTAGGAACAAGACAAAAATGTCTACCTTGGCACTTCTATTCAACATATAGGAGTTCTAT
 CTAGGGCAATTAGGCCAAAAAATAAAACAAAAGACATCTAGGCCAGGCGTGGTGGCTCACGCTGTAATCCCAGCACTTT
 GGGAGGCCAAAGTGGACAGATCGCTTTGAGCCCAGGAGACTGAGAACCCCTGAGCAACATGGCAAAACGCCATCTCTAC
 AAGAAATACAAAAATTAGCTGGGCATTGGTGGCTTGTGTTTGTAGTCCCAGCTACTTGGGAGGTTGAGGCTGGGAAATTG
 CTTGATCCCAGAAAGCGGAGGTTGTAGTGAGCTGAGATCACGCTACTGCACCTCCAGCCTGGGCCACAGAGTAAGACCTG
 TCTCAAAAAAAAAAAAAAAAAAGAAAAAGAAAAAGAAAAAGAAAGCATTAAATTGGAAGAAGTAAACTATCTCTAT
 TCATAGGTGGCATAATCTTGTATAGAAAACCATAGGAATCCACAAAAAATCCATTACAACCTAATAAATGAATTCAG
 CAGTGTTCATGGTATAAGATCAACATACAGAAATCAATTGTTGTTCTATACACTTACGATGAGCAATCTGAAAATGAAA
 TTAAGAAAACAATTTATATAAAATAGCATCACAAAGAAAAATATTTAGGAATAAATGTAACAAAAGAAACACAAGAGT
 TATACACTAAAAATGACAAAACACTGTTGAAAGAAAGATATAAATAAATGGAGGATATCATATGTTTCATGAATCAGAAGA
 CTTATTATTAATAATAGCAATACTCCCCAAATTGATCCATAGATTAAATGCAGTTCCTTCTCAGAATTCTAGCTTGCTTTTT
 TTTTTTTTTGGCAGAAATTAGCAAACCTGATCCTAAAAATCGTGTGGAAATTCAGGGACCCAGTATAGCCAAAACACT
 TGAAAAACAAGAACAATAATGGAGGCTCACACTTCCCAATTTCAAACCTTACTACAAAGCAAAAGTAGTCAAGACTATG
 GGGTTCTGCATATGATAGACATATAGATCAATGAAATTGGGTTAAGAGTCCAAAAATAAATCTTCATATTTATAGTCAA
 TTGATTTTTTGACAAGAGTGCCAAAACAATTCAATGGGGGAAAAATAGAATTTTCAATAAATGGTGTGGGACAACCTGGGTA
 TCCACACTCAAAAGAATGAAGTTGGACCCCTATATTACACTGTATACAAAACTAACTCAAAATAGATCAAGACCTAAATG
 TAAGAGCTAAAACTATAAAATTGTTACATAAAATTATAGAGGTAATCATCATAGACTTAGAAAAGGCAGTGGTTTCTTAG
 ATATGACACACTCGAAAGTATGAGTAACAAGAAAAAATAGATAACTGGACTTCAGTAAATTAATACTTTGTGATTTA
 TAGGACACCATCAAAAAAATGAAAAGGCAACACACAAAAATGGGAGAAAAATTTGCAAAATCAAAAACCTAATAGGGGACT
 TGTATCTGGAATATATATTTTAAATCTTACAACCTCAGTAATAAAAAGACAAATAACTCAGTTTTTTAAAGGCAAAAGA
 TCAGAATAGACATTTCTCCAAAGAAGATACAGCCATAAGACCATGAAGATGTTGAGCATCATAGCCGTGAGGGAGATGC
 ATATTAAAAATCACAATTAATACCCTTGATACCCACGAAGATGGATATAATAAAAAAGACAGGTAATAAAGTGTGGCA
 AGAATAAAATGGAGTCTTCAGACACTGCTGGTGGGAATGTAAATTTGTGCAGCCACCGTTGAAAACAACCTTGCTGATTCC
 TCTAAAAGTTAAACAGAGGCTGGGCGCTCGGCGGCTCAGCCTATAATCTCAGCACTTTGGGAGGCTGAGGTGGGCAGAT
 CATTGTAGGCCAGGAGTTTCGAGACCAGCCTGGCCAAGATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCCAG
 GTGTGGTGGCAGGTGCCTGTAGTCCCCGCTACTTGGGAGGCTGAGTCAGAAGAATTGCTTGAACCCAGGAGGTGGAGGTT
 GCAGTGAGCCGAGATCGTGTCTATTGCACCTCCAGCCTGAACAACTCCATGTCAAAAAAAAAAAAAAGTTAAACAGACAGTT
 ACCATACAAGCCAGCAAAATGTACTCTGAGGTATGTACCCAAGAAAAGTAAACCTTAAACCTTGATACACATACTCATAG
 CAGCGTTGGTAAGTCACAATAGCTCAAAAGCAGAAACAATCCAATGTTTATCAGTTGATGAATGGATAAAATTCACCAA
 TGGAATATTATTTAGCAATAAAAAGGAATGAAGTACTGATGCTACAATATGATAAACTTAAAAACATCATGCTAAACAGC
 AGACCCAGGGTTAGAACACAGGCAGTCTGTTTCTGGATTCTATGTAGTTCTATCCTATATTGCTTGGTTTTCCAGGGTTA
 GAACACAGGCAGTCTGTTTCTGGATTCTATATAGTTCTATCCTGTATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGT
 CTGTTTCTGGATTCTATGTAGTTCTATCCTGTATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGTCTGTTTCTGGATT
 CTATGTAGTTCTATCCTATATTGCTTGGTTTTACAGTCACTCATTGCTTAGGAGCGTTTTTCATCACTCTTGACTGTTT
 AAGAGCTCTTTAGTCAATTTCTTTTACCATAACCTCTTGATTCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG

FIG. 7B (3 of 15)

[illegible]

AGAAATATTGTGTGACCTCCTCCACCTTTCTAATATCCGCTTTACCAAAGTTAGCTGCTTGAGGTGGTATATGCCTTTTA
 CATTATTTGCCTCTAAGGGAAAACTCAAAAGCCCAAAGTTACCTGTTAGAACATAGTCCTTGTGAGGTTGTATCTCAA
 GATTTCCTTTTATCTTGTCAACAACTCAGAATACTAAAGTTAAAGTTGCTTTATAACCTCTATTATTTCCATCCAAAA
 CTAACATTTCCCTCCCATACCCACAAATTCCTCATTGCAATTTACCAGTACATTCCACTGGATATTAGCTACGCTGCAT
 GAACCAAGGGTGCAGCCTCATTGTTGTTGTTGTTGTTGATGAGATGAGTAACAGAGAGTGCCTCAGCACTTTAAATGA
 ATACTTGTGGCCAAAATATTAAAGCAAATAGCCTGAACCCCCACCCCCAGCCCCAGGCAAACATAAATTATGGTTAAAC
 TTCCATTACAGAGAACTCCACAAACATGGATTGATTAATTTGCTGAGCAGTTCATGACCCTTATGTTATACTTTGCACT
 ATGTAACAAAGAAGCTAAATCTTGAACAGCAAGCTTATTCATGGCACCAGCCAGTTTCCCTTCTCCCTGTAAGTCTAAC
 CCTCTGCTGCCAGCACGAAGGAGAAATACTTGGAGATCTTAGCAGCATGAAAGCCTCTTGTATCACTGGGATTGCAGC
 ACGCATGATCAAGGCCAGGGGTGATCACCAGGCCACACTGCTCCTAAGACAGAGGTACTCAGATACGTGGCTGAAAGCC
 TAGCTCAAATACTGCCCCAGGTGAGCCTCTTGTGCTGAGTAGCGCTACTCAAAGAACACAGCTTCCCTGCTAGGGAAGG
 CAGGGCTACTGGCAATAGATCTCCAGCCTAGCAGTGATGTACAGTCATGGTATTTTAAAGAGAACCTTTGAATTTTCTG
 TTGCTTGACTGTTAAAGCCTCAAATTTTCTGTTGCTTGACTTCTTCCCTGGCCTCCATCCCCAATCTGCCTCCCTCAG
 CCCTATAAGCAGTACAACATGCTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCCTCTGGATCATGAAAAATGC
 TGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACGCAGCTCAACAGGATTTTAGATCTACTTTTCATCT
 GTGTGTTATGTTTTGAGTATAAGGTAAGTCTGGAGTGGCACAACCTTTATACCAGCTCTTATCTCTCAATTGCAATTCTGT
 CTTCTTACTCATCCCTTTGTTTGGGCCATGGAGGCATCATTAATTTTTCTCATTTCTGTATTCAAATCCATAACCCATT
 TGTAGGTATAGATATGATCATTTCACAGGGAAGGATCTCTGCCTCTGCAGAGAGAACCCCACTTCTGTTGACAGAGTT
 TTGGCCCATAGGATGCTCCAGAGCAGCATCTCAGTGAAGCAGATGTCAAACCTTAGCTGGCATCACTGTGGAGTGTACTGT
 TTTGGTAACCTCTCCCATCAACGGAGATCTCACCAGGACATGTCTCTACCTCTGTCTTGTCCAGGAAAACAGAGT
 TCTGACAAAGTCAGTACCCAAGTCTGCAGAAGTCAAGGGATGTCAAGGCCCGCTGGAAGAGGCTTTGCTCCGTGGGA
 AGGGGCCAGAGGGGAGATGATGCCGCCCGGGCTCCAGGTGTGTTGAGTGGCCCTTCCCTGCTCTCTGCAAGCAGTTT
 TTCCTGTTTGTGGGGAGGAATGCTCTCCCAACATGATTAGACACCATTACTTTCTTGAGATATTTACGGTAGTGTGAGA
 GACAGCGGATTCTGGGAGTCTGTGTGTGACATTTGTGTTAGCCCTGTGCCTGTGAGGGAAGCGCTGTTCTACAATTGTA
 GGAACCTGAAAACAGCACCAATGACATCTTTAATTAAGCTGTTGATGGTAAAGGTACACCTCTAAGAATGTCAAGT
 TTTGGTAACTCTCCCATCAACGGAGATCTCACCAGGCTGAGGCCCTTCTATGTGACCTTTGGCTAGTCTATCCGGAGCATGGTC
 AAGAACTGAACAGTTCTGGCCCCAAGATCATCTTCTCGATCATTACAGGGCACTATTAGAATGGAACCACTTCCCTGAAA
 TGGCTTCAGAGTGTCCAGTCATTCAAGGATTCACCACAGGAGGAATGATCTCAAAAAGGCTGAGCTTGAATAGAATGA
 AATCCCAGGTACCCCTAGTCTTATTCACCATGCTCAAAGTAAACAGAGTGACAGCTTATTGTATTGGAAGGGACACAG
 TGGCAGGGAACCTGGAGGGAGCTCATAGTTTTCAGTGGTGGTCAGGCACCTCATTTGACACCCATACTTTTCATACCCAA
 TAATTACAGTAAGCCCCAGAGTTTACAGGAATCCTCTGCTCATGAGAAATGTCTCTGACACTCAGAAAGGCAGAGT
 TCTTCTTATATTCTAGTCTATCAATCAAGAGCGGGCCAACCTGGACATAGGTGTGGCGACTTTGTCTCTACCAGCAAC
 CTGCATGGACTCTAATTAGCCCGAGAAATGGTGTGAGGCTTCTCAGTTGAGCTTGTATGAACCTCTGTTATCTTGGGA
 GGGTTTCATGCTAATCAAATTCCTATCATGCTTCTTAACTCCTAGGGAACGACCGATTTCAGGCCCTAAATGAAAATT
 TGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCTAATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCT
 ACTTTTACCTAAAGTCCAAACTATTTTCCAGGCTGCTTGTATTACTGAAACAACACTCCTTCCAGGGTATAGAAA
 ATGAAACATCATTATCTGTGTAATACAATTCATCCAGGAGCCAGGATAATCAAAGGTATAGGGAGTTGTGGTTTCCAG
 CTCTTAAAAATTTGTACATTGATAAGCATGTAAGAAAACTAATATTTCTTTAGCAACCTCAGATGGCTTAATAAAAGC
 AGCTGATTTTGCAGGGAGGGTAGCAGGGAAATAGAGAAAGCAGGACACGGTGCCTAGGACCGTATACTTTCAAATCGATA
 TTTCTTTCTGGAATATGTACAAGATATACATTAGATATATTATGTGCTAGTCTACTTAAAGTTGTTTTTAAATTTG
 AAAACATTCTAAATGCTCCAGAATAGAAAAATATATTTAAAGTTGGATTGCCATCAAATGTTTAAATCATCTTAAT
 GACATGGGGAATGCTTATGACATAATGTTAAATGAACAAAGGCAGGGTAGACACTTGGTTTTCTAGTAGTGTGTGGCTC
 ACGCCTGTAATCCAGCACTTTGGGAGGCTGAGGCCGTGGTGAACCTGAGGTCAGTAGTTCGAGACTAGCCTGGCCAAC
 ATGGTGAACCCCGTCTCTACAAAAAATAGAAAAATTAGCTGGGCATGATGGCAGATGCCTGTAATCCAGCTACTCAGG
 AGGCTGAGGAGGAAGAGTCGCTTGAACCCGGGAGGAGAGGTTGCAAGTGAAGCAAGATCGTGCCATTGCACTCCAGCCTG
 GGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGAACCTCAATCTCTGATGACATATAGTCAATGTATT
 TTTAAAGGCTAGAAGGAAATTTACCAAAATATTAATTGCGGTTTTCTTTGGGTGCTGGGAATATCGGTAATGATGTTT
 TCTCTTTTATACTTTGCTATGTTTCTACAGTAGATGTGATTATAATATATATTGTTACAGAAAAAAATTTATAAGA
 AATGAAAGAATAAAAAAACCTGTTTGGATCAAAATCTATGCTATAGATGAATAGATATATTGACGTGTATTGCTATATAT
 GCAACAATTTAGACATATGAAAGCTAAAAGTATATATGTTTGTAGTATAGCAGATGTTTCCGATACCGTTTAGCCACAG
 GTAGCCTAATGAGTCCCAGGGTTTGTGAGCAAAATGTCGTAGAGCTAAAATCACCCCTCACACACAGTTGACAAGGTAG
 GATACCCCATGGGTGATGAAGCACCCATCAAAGGGGGTATGGGGCAGACTTGATTAGCAGTGTGTTTGTAAATAAATG
 TGAGTTAATATCTTTATGTTTACCACAAGAATGAATCATTCTGGTTAACTTATGGGACTTTGGGGAGTCACATTTATTT
 AAAAGTTTAAAGAAATAAGTATATTTTATTATAGATGTGACTTGGAAACCCAGTTTGTGTTATCATGCCATTTGCTTT
 GGGTATGTTATTCTTGCACTAAATTCCTGGACTGATTTATAAAATACTTGGATCGGAGAGTCCATACATTCTACTTCGG
 GCAATGAACAACAATAACAAATATGATGCCGTGGGTGCTACAGAATTGCTTAGGTGGTTTAGCTCATCTACTCTACTA
 GATTAAGAAGAACCCCTAAGTAGGCCCTGTTTTGCCCTGGGCTGTGTAAACTGGTGTGTTTGGAAAACCTTTCCCTTTGCT

FIG. 7B (5 of 15)

TGCAGGAGCAACACAATATTGGTCCTTACCACGCATGGCCTACCGGTTTGCTCTAGGTTAGTTCTCAGCCCTGCGCTACC
TGGTGGGCTGCTGGTTGTCTAGAGCTAATGATTCACATCTACAAATCTCAGGGGCTTTGTGCTTTTTTTTTTTTTTAA
AGGGAAACCATAGTAAAATTATAACTGTTCAACCTACCTACCTGGAAAATTTATAATTATAATAATGGTGTCTTTCACCC
TCTTTCTGATCATTTTTTCGATTATTTTGGCTCTGTTTCTTTTAGAGCAATGATCTTCAACTTAGGCTGCACATTAGAATC
ACCTGGGGAGCTTTAAACCTGTCTAGTGGCCAGCTGCACCTTAGACTACTTCAATTGGAACTCCAGCAGGACCCAGAAA
TCAGTATTTGGTAAACTTCCCAGGTGATTCTATTGCCACCAATCCATTGTTTTAAAGGAATAGATGGTAAGCTTTTCT
TTTCTTTTTTTTTTCTTTTTCTTTTTTGAGACAAGGTCTCACTCTGTCAACCAGGCTGGAATACAGTGGCACAATCACAG
CTCACTGCAGCCTTACCCTCCTGGCCTCAAACAATCCTCCCACCTCAGCCTCCCAAGTAGATGGGACTACAGGTGTGTAC
CACCACAACCTGCTTACTTTTTTGTATTTTTTGTAGAGACAGGGTTTACCCTATGTTGCCAGGCTGGTCTAAACCTCCTGGG
CTCAAGTGATCCACCTGTTTTAACCTCCCAAAGTGGTGGGATTACAGGCATGAGCCACTGCGCCTGGTCTAGATGGTAAAG
CTTTTAAAAAACAGATTAGTGTTAGTGATGGTTGCACAATATGAATGTACTTAACACTACTGAACTGTATACCTTACAAA
TGGTTAAGATGGTAAATTTTTATGTTAGGTGACTTTATCACAATACAAAAATTTGGGAAAAACAGATTAGGACACTCT
AGATTTGTGCTGTCCAATACAGTAGCCATTAGCCACATGTGACTATCAAATGCTTGAAATATGGCTAGTTCAAATGTAGA
TAATAAATCAAGATAAGTGAAAAATACGCACCAGATTTTGAAGGCTTATTGTGAATAAAAGAATAAAATATTTCACTAGT
AATTTTTATATTGCTTACATGGAGACAGTATTTTTTATCTTTTAGGATAAAACAAAATATATTAAAAATAATTTCACTTTT
TCTTTACTTTTTTAATGTGGTTACCACAATATATAAAATGACATATGTGGCCCCCATTTGTTTCTACTAGACAGATTGCT
CTAAATTTAAAACTAAACTAGCAGTCAATTAATTAAGGATGATAAGGGGCGGGCAGTGGCTCACACCTGTAATC
CCAGCACTTTGGGAGGCGGAGGTAAGTGGATCAGGAGGTGAGGATCGAGACCATCCTGGCTAACGCGGCGAAACCCG
TCTCTACTAAAAATACAAAAAGTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCAGCTACTCGGGAGGCTGAAGCAGG
AGAATGGCGTGAACCCGGGAAGTGGAGCTTGCGGTGAGCCAAGATTGCGCCACTGCACTCTGCACTCCAGCCTGGGCGAC
AGAGGGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAGGATGATGAGGTTAAAATGGTAAATTTGATGTTATGTGACT
TTATCACGATATAAAAAATTTGATGGCTCATGCCTGTGGTCCCAGATACTCAGGAGGCTAAGGCAGAGCATCACTTGAGCC
CAGGAGTTTCAGGCTTCAGTGAGCTATGATAGTGCCACTGCACTCTAGCCTGGGTGATAGAGCAAGACCCTGTCTCTAAG
GAAAAAAAAAAAAAAAAAATTTAGATTTCAATTTATTTTACACATATATTATCACTTGAAAAATGAGAAAAAGTGTCAAG
TGGCTTGGGACCGAGAGCCTATCCTAAACATGAAAAACAGTAAACACACAGAAAGTACTTATTTTTTGAGTCTCAGTG
GTATGTAAGCAGCTGCAGTGCCCCCATTATTAGGTAAATGGGACGCAAGAACAGGTAAGTGGTAACCTTGGCCAGGACA
TATGAGCTGATATAATGATACCCCAACCCCATGGTAACATCTTGGCTACTGAGGCATCTTGGTAAAGTCAATTTCTCATA
CCTCCCTTTCTTGCAACTAGATTTGGATGATGATACAAAATATCCCTTTACAGCTTCACTTAGATTTTATAAGAAATGGA
TGGGCTAGCAAAAAAAAAACCATTCTGATTCCCTAAAGTGAACCTAATAGAGGAGCGAGCACCAGGCAATTTCCCATTTCC
TAGTGGGCAATGACCAGTAATGTCCGGCAGGATATTAGTACCTGCCCACAGGAATACAGTCTTGTTCCTCAATGGAA
AAGGACGAAAGACCCACGCACCTTGGCTGAGCAACCTCAAGGTGATCTTTGGGAAGTTAAGAGGCTGACTCTCCCTGAC
TTGGCTCTGAAGCTCCACCCTTTCTAACCAGCGCATCACTGCCAAGTTCACATCACATCCAGTCTCACTCTCTCTCG
CATGTTGCAGGGGCTTCCCTTACTCAGATCTAGCAATGGTTTTTCATGCGTGAAATACAGCCATGGCCTGAGGCTTTAG
GCAACAATCTGAGAGGGGAGCTTAATTGCTAGTAGCAACTAATAACTGCTTCTCTACCCATAGTGTTATTTTTATAATTG
TCCTCATCATTATTAATAATAGTGGGATGAGGATGACCAGGAAACCTTACCTAGACAGTTGTTTCGACAAGACATGAAT
CACAGAAGGCACCTGCACTGTAGTTACTCAGGGCAGTTGCTGTTTTTCATTTCAAGGTTGACTATTTTGGAGATTTCT
TTACACCTTGGTGATAGATTGCCATCATGGAACTGGCCAGGTTTGACATGCGCTTAAATTTGACCTCTTGTGTGTTT
CTAGAACAAAGGCCGAGTTAGATCAAGAAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGAT
ATGCAGGAAACATTATCCAGGTGAGGAAACAAACACCAATCTGATTGTTGGCCATGAATATGTTTACTAGAATAAG
GACTTCTTTATGCAAAATTTGTGAAAGACATAAATGTGATCCCATAGTACCTTTTTTAAAAAATGAAGTTGAGAAGTTTA
CTATTTACAACAGTGTCTACCTTATAAATTCAGAGATACCAACATTTCTTGGCTTCTTTGACTTAGGCTTACTTGG
AGAGGTTAGGTGTTTGGCCAGCTGACCCCTCTGGTTAAATCTGTGTGAGTATGTACCAAGTTTATAATATGATGTTGG
GTTTTATCGTTTAGTATCTAGAACAGTAGTGGTAAGTAGAATTTTTTCTGATGGGTCAACTCCAGTTGAATGATGGTCACT
GTCTGATATGGGAGCTATGATTATGACTAGGCTAGGTAAAAAGAGTGCTAAATTTGACAAATGATGTCTTCTTGGACTT
AAATTTGTTAAGGAAAGTCATTGTACCATGAATTTGCCATCCCTGCTGTAGAAAAATATAGCTTTGTGAACTTTGTACC
ATACTAATTTTATCTTCTATGTGATTATTTCCACAAATTTCCCAAGCTGTCTAGGTAATAATGAGTTTTTAATACCTGA
AAAATGAGTTCTTACATGTTTCCATTGAGAAGTCATTCTAGAGTAGGTCCAGGATTGCTTTTAGGGCTAGAAGAATA
TCGTTGAAACACAGTGAAATCTTAATCTCTAACTTTTGATTTGTCTAAATCAAAGTAATCATCATACAAAAATAAACA
CAAAAAGTATGTGATATTTTTGTTGACTTTAATATCTTTGATACTTAAATGCTTGGTATCACATTTACCTTATCTTTAT
ATAGCACAATATTAGGTGCCAAATATCTATACTAGCCCCAAATATATTGTCAGTTTTCAAAGAAAGCTGAAACCTTTG
TTATTATCCTTGGTGTGTTAGTCTCTGTAGGTGATAACAAGCTTCTATTTAGAAACATTGCTGCCACCAAGCAGCC
CCTGTTGTACTGGGAAGCCCAATTTGTGTTTTGCATCCCATAGGAAAGCTATGTCTTGTATACAAAGAAAGAACTTTC
CAAAAGATGTGACCCAGGATGAGGAGATGGGCTTATACCTTCAATTTAGGAACCCAGAAATAGGTATAATCCCAACT
CATTGGAAGCATTGAAATAAAGCCATTGGAATAGGTCTTCAGTTCCCATGGTTAATGGATGATACCCATGGTGGCTCA
CCAACTCTTAAGACTCACCCTGGACATGGAACATCAGCATTACTGAGCTAATTGTCAGGAACATCCAGTTCAATTGGCA
CAGTGCAGGGATTCAATGATGCTGTTCTTCCATTCCCCAGCGAGCTCGGCTCTGGACTGTAAAGACAGCCTGCTGGGA
GGTGTCTGAGGGTGTGGTGAATTTCTCTGAAGTGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCG

FIG. 7B (6 of 15)

TGCTCTCATCGCCAAGGTAAACTTGGGATGCTTGTCTTCTCTTAATTAAGAGTAAGATTCTCATCTAGCTTCATAC
TTCTCTCTTCAGGTGGACCAAAAGTCACAGAGCATATTAAGTGGCATCACAGTAAAGGTCTTAAGTCTTCTAGGAAGAA
AGCAGATGCCCTGATTCTGTGGGAAGCCACCATGGAGAGGAAAGCAGTGGCTCCCATATTTGAAGTGTGGACCTAACTC
TAGAAGTTTAAATGGCCATTGCTGAAGTCTATGACATGAGAACAGAGATCAACTGAGTGACTTAGCAATTTCACTCT
TTCTCTGTAATACCTCTGCTGAGTGAGATTAAATCCTCTATGTGACGCCCATTAGTCTTACAAAATGTCATGCCATAAAA
TGCCAGGAAGGTGAGAAATGAATTTCTACGGCCTGAGGAATGAGGATTATCTGGGGTAACATGCAGATTATTTTCCC
TTTATTTATTTATTTATTTATTTTGGAGACTGAGTCTCGCTCTATCGCCCAGGCTGGAGTGCAGTGGTACCATCTCAGCT
CACTGCAGCCTCTGCGCCCTGGGCTCAAGCGATTCTCATGCCCTCAGCCTCTGAGTATTGGGATTATAGGCGTGTGCCAC
CGCACCAGCTAATTTTGTATTATTAGTAGAGACAGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGACCTC
AAGTGATCCACCTGCCCTCAGCCTCCCAAAGCACTGGGATTACAGGCGTGAGCCCCGTTCTCGGCCATTATTTTCCCTTTA
TTGAAGATCTCAATTGGTGCCCTTCTACATGGGGCTTTTTAAATTTAAAAAGTAAATTTCTCTGCTCATCTTCTCAGGA
CCATTTTCTCTTTCTTCATCACCAGTAATTTCCAGGAACCAAGAACTCAGGTTTCCCTCCATCATAGTTGTGATTTC
ACCAGTGAATGCGACCTGGCTCAGAGTGCAGTTGATAACACAGCTCTGACCTTTTAGCTGGACAGTTCAATTATTAATC
TCAAGTCTACTCCATTGCTTAAATCCATCTTCTGATTACATAGCTCATTATCTTTATGGAATAATGCATTAACTCTTCT
AGGCTTTTGTCTTGTCCAAATGGACATTTGCATATTTCAACGGTCCAGAAAGTGTATCAAACTGCCAAGTATGCCATAAT
GGCCCTTTATGTCTCTCTAGTTTGGAGACTTACTCTTTGAAGAGGAGGTGGAACAGTGTTCGACCTATTTTCCCAAGT
CCTGCACCACTGCAGCAGCAGCATGGATGTACCCGGAGCCAAGCCTGTGCCACCCTTTACCTCCTCATGAGGTTCAAGT
TTGGAGCCACCAGTGTAAAGAGTTCAAACAGCTGAGTGACCTGGAATCAGTAGAGAAAAATTGATGTAAAGCATCAGCTG
CGAAAAAAATAAGGAATTTTGCAGTATTGCAGTTTACTTCTGTCTGTGAGAAAGAAACAATTGAGTATGTAGATAGA
TAGCAGCTTCCATTTTAAATTTGCATCTAAAAGTGAATTCATCAGATAAATGCAGTGGTCTCTATCAGTGTGTTCTAAAA
TAGACAGCCAGGGGCCAGGAACGATGGCTTTACCTATAATCCAGCACTTTGGGAGGCCGAGGTGAGTGGATCATTGGA
AGTCAGGAGTTCAAGACTAGCCTGGCCAGCATGGTGAAATCCTGTCTCTACTATAAATACAAAAATAGCCAGATGTGTTG
GCGCATGCCTGTAATCCAAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCAGATATTGCAGTGAG
CCGAGATTGCCCCATTTCACTCCAGCCTGGACAACAGAGTGAGACTTCATTTCAAAAATAATAATAATAATAATAATA
ACCAGGTGCAGTGGCTCATGTCTGTAATCCTAGCACTTCGGGAGGCCAAGGCAGGCAGATCAGATGAGGCCAGGAGTCCA
AGACTAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAATACAAAAAATTAGCCGGGTGTGGTGGCACACACGCCCGT
AATCTTAGCTACTGGGAGGCTGAGGCACGAGAATCGCTTGAACCCAGGAGGCAGAGTTGTAGTGAGCCAGATTTGTGC
CACTGTATTCCAGCCTGAGACCTGTCTCAAAAAAAGAAAGAAAGAAAGAAATGGAAGAGTATTTTAGATTAAAGTT
ATCATCTGTGGGGGAAAAAATACAATAGACAGGTTAGAATTCAGAAGAGTGTTCCTGTTTCTAAATTTCTGACTAGCTAG
TGCCAGAATGACCTGTGGAAGAGGATTTTAAATGATCGGTGTCTATTAACCTGAGTTTTATTTTAAATATTTATTTATTT
ATTTATTGAGACAGTGTCTGTCTGTCAACCCAGGCTGGAGTGTAGTGGCACTATCAGAGCTCACTGCAGCCTTCAACTC
CTGGGCTCAAATGATCCTCCTACTTCAGCCTCCCATGTAGTAACCTGGGATTACAGGCACGAGCCACCTTACCCAGCTAAT
TTTTTTTGCAATTTTGTGAGACAGGCTTGTGCTGCATGCCAGGCTGGTCTAGAACACCTGAGCTCAAGTATCTTCCC
TCTCAGCCCCCAAGTACTGAGATTATAGGCATGAGCCATCTGCCTAGCCAAGACTTGAGTTTTATTCAAAGCTACG
AAGACTTTGGAGTTCAGCTTTATTATAGAACAGTCAAGTTTGTCTTAGTTTGTCTAGATTTTGATACCTTCTTTGGAATT
TCCATTTGTGGCCATGTTAATAAGTATGCTCAAGTGATATATAAGATAAATTGGCCCATGGAAAAAGTCAGCCTCCTC
CAAATGTATTAGGGATGATTATTTAAAGACATTCCTCAGGGGACCTTGAGGTAGCCATGTTTTTCCATGGGCCTGTAA
GAAAGAAGAAACAAACCTTGTGCTTACCCGGAGTTCAAATCTCAGAAATGCTGGCCACAGAAGTCCCTGATTATT
TATTTAGAGACAGGCTGTGCTCTGTCAACCGTGGCTGGAGTGCAAGTGGCGAGATCTTGGCCCATGCAACCTCTGCCTAC
CAGGTTTTAAGCAATTCCTGCCTCAGCCTCTCGAGTAGCTGGAATTACAGGTGTCCACCACCATGCCAGCTAATTTTT
GTATTTTTTAGTAGAGGCGGGTTTTGCTGTGTTGCCAGGCTGATCTTGAACCTCTGAGCTCAAGTGATCCACCTCCTT
GGCCTCCCAAAGTGCTGGGAGGCTGAGCCAGAAGTCCCTTTCTTTAATAAAGTTTAAATAAAGTCCCAAGAAGAACTC
TTGGCACAAAAGGATATACTGTATCTTGGACCAACTTTATAAGAATCTTCAGCTTGACAGACAAAGGCAGCCAGTC
CTCAATGAAAATTTAAAGGGAGCCTGACAGATTTATGTGAGAGCAATGTCCATTTAAACCATTAAACAACAATATGAAT
GTTGTGCAAAGTGATGCTCCCATTTCAATTGAGAGAGAGGAAATAATTAAAGCGGGGCAAGGAAACACTGAGGAGTTGT
TTGTGTCTGGCCATGCTGCTTTCAGTTATCTACTGCTAAGTGTGCTTATTTACTTCATCTTTTTTTTTTTTCTACTGA
TGCAGAATTTTGAAGAGTAAAGATGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAATGAA
GAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTGAGAAGAGGACACAGCCATGCAGATGACTCCTTTTCCAC
CCAGGTACACCGAAGCACATACCTTGCTCATGCATGAGTTTGGGATCTGCCAACTATTGTGTATGTATGTATGTACATA
TATACAAATTTATATATAAATATATAACATTTGCAAGTATTTATTTGTTCAATATGCATGTGCTCTCAGCACTCTGAGAG
GTTTTTAAAGAAATACATCCATCACTGTCCCCAGTCTCAATATGCTAACAGTCTATTTGGAGTGCTCAGTCTCAAAACA
ATTAGGAGGCAGTACAAGACAAGTGATACATAAGTGCAAAGTGTGTGGTAAGGAGCTAAATGCTATGGAAGGTTAGAGGA
AGAGAGGTGCTGATCAATAAACAATCTGGTGGCCAGGAAAGCCTGCAGGGAGGGATGACACTAAAGGCTGGGGTAGGATT
CCGCTAGGCAGGGGAAAGTGAGGGGGAAATTTGTGAGTAGTTGAAACAATGAATGTTTGTATCTGTAGGGATGGTAAAG
GGACAGCTTGTCTGGTGGGGTAAGGAAGGGCCAGTTTGAGAGAGCTTGTAAACAAGGTTGTCTTAAGGAAATGTGT
AAGGACAGTCATCTCTCCATGTCCATTACGATGACCGTGAAGTCTAGCCTGTCCATTGTCTTTTAACTCCAGCTCC
TAGCCTGTCTATGGTAGGCTCTTAATTAAGTGAGAATGAATGAATGAATGTTTCTTTTATCCCTTAGTCTGAGAACC

FIG. 7B (7 of 15)

CTATTTCCGGAGTCTGTTTTGCCCTCTCGGGCAATGTTGCATCCTCATTCTCAGAATCTTTTCTCTCTCTACATCAA
 ATCGTTCCCTCTCTCATTTTCATCTTGACCATACTCCTTTAGTTCCATCATTTATATAGAGGTATTCACCAACAAGACCAAT
 CAAACTATGGGCAGTTTAAATAAAGGTCTTCAGTGCCTTCACCCAATGAAATGACTCTAGTGGTAGAAATTTTAGGAGCCC
 TGGCAAGCTGGCAGAGGGGAACGGGGATAAGACAACATTCTGTGGCTGAGTTACCTGCCAGGGTCTCTAGATCAAGCCAT
 AGTCTCTCCCTGTTTTGTACTGCAGGCTCCCTGGACCTCCACTGTTGGTTTTATAATTAAGAAATAAATGATTACAAGA
 GGTTCTAAAATCTCTGAAGCCCTGGGAAGATCCAGGAGGCTTCTGAGACATGGAACCTCAAGCTGAGGTCTTAAGCTGCTT
 CCTACTTGGTATAAAAAATCCCTGATATTCCAGAGTAGAGTTTGAACCTTTTCAGGTTACAAATAACTGAACTGGTTCAA
 ACTAATTTAAACAAAAATGTTGGAGATAGAGATAGTATGAGGATTTCAGGCAGATTTCTGGATCTCAAGGGCCAACACACA
 TCCAGGTCTCATAACTCCTGGGCTGGCGAAGATGAAAACCTACAGAGTCAGGTCTAGATGACTCCGCCATCCCTAGTCTC
 TGCTGCCCTCTGATCCAACCCCTCCCATGGCTTCCCCTTGCAATTTCAATGTAATCCTAACTCTTACCTGGGACTACAAA
 GCTAAGATTATTTTGGGCTTACACTTTTTTGAGGTGGAGAACTTCTCTGTAATCTGAATAGCATCTTATATGACACAG
 TGAATGAGGGAATTTTCAGGAAGATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCTGACACACTCAAGG
 GACACCATTGGGGGTCGAGGATTGTCTACTGTGGAGTTCTTACTAATGTAATGATCAGCTAACATGGATATAGTGAT
 TTGGATGATAGCCAAATAATATATAGAAATTAACATTTCAGAGTAGGTTAATTCATATGTAAGTTTTTCAGAAGGATCTCC
 CTAATTTAAAGTGAGGCATAATAATGTTATTAAATATAATAACATTATTAATATAATAACACTATCTTCTACTTACCAC
 AGAATCAGAGAAAGAATAATTAAGTGTATAGGAATTATTTCCATATGCTTTTGTTCGAATTATATTCAGACATACATA
 TATAGTTTTTGTAGAAATCATTTTTTACGCGTAGTTTTAAAGTTGGTCTTCCAGTCCCTGTTTCAGGAGAAATTTACTTA
 CAGAGGCAAAATTTCTGTATGCAACATCATACAAAGGGCAGTACTTTTGTCTTCTGTTTTATTTTGGAGAAAGGAAAG
 AAAAGGCAGAAATTTGCTGAGAGCCATTAAATAGACATCATGTTATCAGGTATTTTTTCCCCATAAGGCTTTTACTAA
 GTACTATTTCTTGGAGGTGAGCAGCTTAAACATGGAATAAAAATAGTTGGACTAATAAATGTTTTCTTCTGTCTCGTT
 TTCTGGAAATATAGGGCAAAATCTCAGGTGGAGGGGTACAGGGAACCTCTTGGGGAGAAAAAAGAAAGGTACACAAAAG
 TAGAAGAACAGTGTCTTAACCCACTGTCTCAAACTACTTCTCACTCAATCTGTCTTCAAGATTGCAAGAGTTACCA
 GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACACACCAAGAAGAAGTGCTACACGGAGGCTG
 CCATGTGCTTGGTGCACGCCGCTGCGTTAGTGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGTGGGC
 AGTGTGAGCTTCCAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTGGTCTCAACTGGGGCGATTTTGTCCCCAGC
 CCCAGGACATTTGGCAATGTCTAGATACATTTTGGTTATCACAACCTGGGATGGGTGAGTAGGTGCTACTGGCATCTGA
 CTGGTAGAAGCCAGGATGCTGTGAAACATTCTGCAATAGGAGAGCTCCCTGACAAAGAATTGTCTGGCCCCAAATGTCT
 GTAGTGCTAAGGTTGAAAAATCCAAGTTCATACATTACATTGCTTCTTCTAATTGCTTTCCCATCGTCGTTGGGTTTT
 TTTTAAATTACTGTTTACAATAATGGCACCTAGCCATTATTAATAGCACTTTAGGAGACATTTGCAAAACATTTACATG
 CATGGCTTCATTGAACTCCCGTAAAGCTGTGAGGCAGGTAGGTAGGGAAGGCGGTTATTATTTCCCACTTCGCGGATG
 AGAGAACTGAGAGAGCAAGTTTTCTAAGGTCACTTAACTCTTTTTCAAAGACTGTAGTTGACACAGTATACTGACATT
 GTGAAAGTTTGGAAACATTGGATAAATGATTTTCTCCTGCCCCATTCTATTGATTCCACTCTTCACTTTTATAGGGC
 CCCTCTCCAATCCAAAAATCAAGAAAGAAATCAAATTGACCTGAGAAAGGAGACAAAAGGCTGAATCAGTACCTTCTTAG
 GATAAGCTGAAAATTACCCACATTTGGCAAAGGGAATTTGCTGCCAGACCTAAAGCTGGCTCGGATGGGGGTCAG
 TGGCCACTTAAAGTGTCTTACTGAATAGTTTAAATAGTCTTTAGAGAGAGAGAAATAAAAAAGCACAATGTTGGGTACT
 TTTTTGTAAAGAGACATAGTTTGTAGAGATGACCATCCCTGAAACCATGAACAATATAGCTACAGTAATAGAGTGTTTTT
 CAAGCCAGACTCACGAAGTCATTACAAGGGTTGTATTATCTTGTGTTGAATTTACATGGCTGATTTATGAAAAGCTT
 TGTCTTGTATTGTTCTTCAACACAATTTTGTGATGTTGTATGAACCAGAAAGAAAGAACAAATTCAAAGTAGCTTCCCC
 AGGCTTAGAGAATAAGTCACTGAACTATGCTGGTGCAGCCAAAGAGCTTCTGGTTTTCCAGAACACAGCAAAGCTGGGTA
 TTGCTCCTATGAATAACTCCTCCTTTCTTATGGTCCCTCAAGAACAAAAATAGTCATTCTGTGATTTTCTGCTTGGCAAA
 TGAATTTCTTCTTAAATTCAGAAATGTTTGTATATAAAGCTGATAATTAATCTCATCCAAAAGCATAAAAAATAACCTT
 GATTTCAAATCACATAGAAGGTGACAAGAAAGTTATAAAGTTATTTTAGATGTATTGCTTCTTTTCTCAAATTTATTT
 TGACCATGTGATACATCAAAAAATAATATTATAGTACTACTCTTTCAATCCCAGGAAATTGTAAGGTTTAGCACTTCA
 TATTGTTTCATTTACTAAATATTTTATACCTCTTTTATTCCTTTTCCCATGACTATATTTTATTTTATATTTATCACTT
 AAATATCAATTGCATTTTATTGACTTTTATATTAGTAAGCCTTACTGTTCTAATTTTACCTAGAATTCAGTTGATT
 TGCTAATAATGACATGCCAAAGTGAATCATTATTACACAATCAACAGAAATATTCCACATTATTCGACATGGGGGCATA
 CAGCTCTATCTGTTACATATATTTATCCATTGATTCTTCTTTTAGAGAATATTTATTGAATACTTATTCTGTCTCAT
 GAACGTTACATTTCAACCAGAGAGACGTAATATACTAATTTATCCAATCTTGTTCAGTTATAATTATGAGAAATACTG
 TTATAAAGAGGCACAAGATATTGTGAGCATTTTATGGTCCAGGCCCTGTGGGTGAGGGAAGGTTGAAGAAGGTGAAAAGGA
 AGGCAGAAGAACTGAAGTGTGAGGGCTTCTTGATGTAGAGGAGGCAATGAGTTAGGTGTTGTGAGCTACAGAAGAGAAG
 CCAAATTATATTAATGTGATGAGTGAATTTCTTCTCAATGGGACATACCAATCAATTTGGAAATGTAGCTGG
 CAAGTGAAGGACACCAACCCAGACTGACAGAAGGTAAAAATGGAATTTATCAGCCCGCTGAGGAATGTGAGCCTGGA
 GTAGCACCTGCCATACTGGACCTAGGGGCCCAACAATGTCAGCAGAGCTCACTGTCATCACCCTTCCCATCTCTGCCA
 TCTGTTGTGTCAGCTTCACTTCTCAGGCTTCCACACCACAGTTTAGGTTTACATCTCTAGGTTCAAGTCTAGGAGAG
 AAGAGAGATGCCTCCTTTCTAGCAGTTGCAGAGAAAGCCTCAGTGCATCTTACTGATCCTGTCTGAACATCTGATCCTGT
 GCTCATCCCTGAACCAGCCATACTGGCCAGAGAAATGGAGTGCTCTGATTTACTGACCCCGGCTCATGGTCCACACCTG
 GAATTATGGGTGATTTCTTCCCCTAAATCAGGATGCCTTACTTTATAGAAGGAGGAAAGAATTCTAGACAGCATTAACAA

FIG. 7B (8 of 15)

CAGATGTCCAGTGTTGATTTTGCAAATGCTCTGTGCTTTAATTTTCAACCTTGTCTGCTCCAATGAAATAGAGCTTTTG
 GAAAAGATTTATAAACTAGAGATAAAATAATATGTGCAAGGAAAATAACTTTGAGGTCACTGAATTCAGGAACTGAGA
 TCACTGAAATTCTGTGTCCAGAGTGCAATATTTATTTTCAACACTGTAGATACGGACACATTCTTAGATACTGCTGTTAC
 TTGTACCTCCCTGATCCTGAAGCCAGAAAGTCTGCAGAAATCCTTTTCTCTGACTACAGCTAATGAGGCTACATAGCTT
 CAAATCTGTTCTCTAATGTGGAAAATTGCATACATTCTAATAGTATTAGTATCTTGGGTTATTAAATGCTTCAACTGA
 ATTTCTTGGATCTTCTGTGTGCACAGAAACATCATAATACATAGGGCAGGTTTGGAAAGAAAGACTGGCCACAAAGGCTTT
 GAGAGCCTCCTCCTATATTCTCTAAACTACGTTACAGTATTGCATGTGAAGAGATAGGGCTATCTATGACAACTATGTCC
 TGACTGATTGCTAAGGTTGATTACATGATCTTGCTAACCAGGCCAGAAGGCAGACAGCTTTTAGTTTACAAGCCAACTC
 TGATCAGTTAGTAGTGGCTGACTGGAGAATATGCTTAAGAATTTTCGAGACTATGTCCAAGCTCTGGGGAAAAAGTGCTA
 CAGTTGATTAGTTATGCCCTGCCATGATTACAGCAATAGGAAGGAGTGGCATGTGTGCCACCTGTTTGTAAATCCCTAAACT
 GGGAAAGGTTTCCCATTTCTTCTGTTTTTCATATGCATTTCTTCCATAGCTGTGAGCTAGGAAGAAAATGATTCTTGACCT
 GTCACATATTCTACTGCCAGGGCCAGTGCTAGGGTGAAGAGGCACTCACCTCAGGTCGAGCGGGTACAAGATCAGTACT
 TCCATGGCCCTAAAAGCGAGTACCTCTCTAAATTTTGTCTTGGGTTTCTCATTTGGTTTACCCCAACCATGGTCTCTGCA
 TGCTCTGCTAGAGGCTCTAAACGCAATAGTTTATGTAAGGAAACAAAATGCATGGAAACAAAATGTTTCAGGAAGAACAAA
 AACACACACACAGTAGTCTGCAATGCCATGAAAACCTTCCCTAATGAAGACAGCCTCGCTTGTCTGTTGTGCTATGTAT
 GGCTGTTTTATCTGAGTCAACTCCAGAGTAGCAACATACTTCAGAAAAACACCACTGTAAGTCAGAGGTCCACTCGGTGAA
 ACAGGGAGCCTAGTTAATGTTAATTGGGTCTTTGCCTTTTGAAGAACAGGACACAGCCCTATGTCCCTTAGGGTTGTTT
 CACTAAAGTAAGTACAGCTGTTGTGACATTGAGGTAAAGTGCTCTTTATACAAAATCTCCTAATGGTTAAAAAGAAAAACGT
 GAGGTTTGAAGACCACTTGCTCAGTGCCTCTTCTAAATGAATGGCAGACAGATACTCTCGGGGTAGAATTACAGACCT
 AGTTTAGTCAAGGTTCTTGGTAAGGATCTGCACACCACTTCTCGTTTCCCATTCGGGGTTCTGTGGTCTCTTACTAG
 TCTGGTCGCCCTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCTGGAGGAGTCTGTGGTC
 TCTGAGGACACCTGTACCTGACGAGGATGGGCTGTGCGCAGGCCAGTACTTACCGAGAGTGGCCTGGTAGGCCCTCCT
 GGAGCAGGCCCGGAGCTCTTACGACGGTCACTGCCAGAGGCGATCCCGGGCTGGCCTCCCATACTCCAGCTGGAC
 TTGGGGTGTGGAACACCTGGTCTTAATGGCCAGTCAAGCCCACTTCCCAGGACACGTGCCAGGGTGTGCGGGGCAG
 GGGATGGGCCCGGGGAGGACTTTGATGTATGCAATTGCATGAGCTTCCAAGGGAGCTGAGATAACCTTTCATCACAGT
 GCCGATCTGAGCTTCACTGTATGCTCATTGGTTGGGCAGCAGTTTTCACAGTATTATTTCTATTTAATAGGGGTGGAAC
 AGCCACAGAGAGGTGAAATGGCCTGCCAGGGTTACACAATAAATGATGAGGCATGTTTTCTACTCCCTCGTTTTTCTCT
 CAGAGAGAAAAAATTAGGGAGGAACCACTGGGAGGAGAGAGGAGGAATACACAGACAGTGTCTTCCCTCCTAGCCACTG
 TGAGTCTGAAGGACATCACAGACCAGGACAGCTTACAGAAATGTGGGCACAGAAACCACTGAGACTCCTCTGGTTAA
 CGTAATCTGGATCTAAACACTCCTAGTATATATACTAGAAAAATATATAGAGAGATGAAGTCATTGAGATTACAGGCAAA
 GAGGAACACCTGTGTCTATTCTTCTTTTCTGTTTGGACAGAGTCTAGCTCTGTGCGCCAGGCTGGAATCGAGTGGTG
 CAATCATGGCTCACTGCAGCCTCTACCTCCAGGGTTCAAGCAACTCTCTGCTCAGCCTCATGAGTAGCTGGGATTACA
 GGTGTGCACCACCACACTCGGCCAATTTTTTGTATTTTTTAGAGGAGACAGGATTTACCCCTGTTGGCCAGGCTGGTCTCA
 AACTCCTGGCCTCAAGTGATCTGCCATCTTGGCCTCCCAAGTGCTGGAATACAGGTGTGAGCCACCACGCCCCAATT
 GTTTTCTATTTAATAATCTCCCTCCTCTTACATTTTAAAGCAAGAAAGTATTAGTACTTTTACTATATTTAGCTGACC
 CAATTTTGTCTTCACTCTATACTATCTCTTATTTTCCAGTTTATTTTCCAAAGTTTCTCTCAAAATTTTATTTA
 TTTTAATTATGTTTTAACTGTCTCTCTCTATTCTTGTCTTCTTTTCAAGATTTCAGAAAAATGTCTAATATACTCTCAT
 TTTTCTTCAACTCAACAAAATGAATFAGAATCTACTACTCTTTGGAGGCATACATTTAGCATCTGGCTAGAGGAGGA
 CCTCTGATGAAATTTAAATATACTAAACTGCCTTTCTGAATTGCTGTAGTCCCTGCTACCAAACTTCTCTCCTGTTTT
 TTCTTTTCTGTTTTGTTTTGTTTTGTTTTGTTTTGAGGCAGCGTCTTGCCTTGTCAACCAGGCTGGAGTGCAGTGATG
 CAGCCTTGGCTCACTACAGCCTTGACCTCTGGGCTCAGCCTCCACCTCAACGCCCCAAGTAGCTGAGGCTACAGGAGC
 ATGCTACCACACCTGGCTGATTTTTTTAATTTTTTTGACAGATGGGGTCTCCCTATGGTGTCTAGGATGATCTGAACCTC
 TGGGTTCAAGTGATCCTCCTGCCTCAGCCTCCCAAGTGCTGGGATTACAGGCATGAGCCACTGCACTCAGCCAGTATTT
 TTTTTTCCCCGAAAGCTCTTCTCCTTACTTATCGCCATACAGGACTACTTAGCGAGGTGTCTAGTTCAAGGCT
 ACCACTGTCCAAAAGTGCTCAGATACCCCTTCTTGCCTGTGAAATACTGTGATACAACAATAAATCACTCTCCAGCA
 CATTTGTTTGGACAATGACCTCTGGTTGCTCTTCTAAGTTTCCAGTGGATTAAATCTCTCTGATGCTCTTCTCTCTTT
 CCAAGGGAGGCTTATATGAGACAGTTAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAAATCCGG
 AAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCGTTAACAAGGTAGCCGGGGAGCCTGGCTGGCA
 GGTCTGTTACCTGGTGGCAGGCGACCTGTCTACAGATGCTTAGCCATCCTTCTCTCCAGGAGTGATTATCTTTA
 GCACATTGCTTTTGTCTCTACCTGTCAAACAGAAAAGGGCTGAAATTTCTTAACAGAGGACCAAAATTCATATGTGAA
 AACATACAGCTTAAATTAATTTATAACCAGGAAATGTGAGAAATTTTAAAGTGTAATTTAAAGAGTCCCAGAAATCTTT
 CATGGGATTTCTTTTGTGTTTATTTCTGAAGTTTATTTCCATTAAGCATTAATTTTTTTAAGGAGTAATTTCTGTTTACAT
 CAGCCATAGGAGTAAAAATGCTTTGTTAACACAATGAGAGACCCCTGCCCTTTGCAACTCAGTGGCTCCTCAGGATGACAT
 AACTAAGGAGAGCTTTTTATATTTTGTCTCCTCAGGATCATAAGAGAATGTTTGGAACTACTTCCGAGTTGGTTCTTTG
 GATCCAAATTTGGGGATTGGATGAACAGGAGTTGTCTACAAAGAGCCTGCAATTACCAAGCTCCTGAGATCTCACAT
 AGACTAGAGGTAAGAAAAGTGATTCTGTGCGCTGACCTGGTACACTTTACAAAACAAGTTAGAGTGGGTCACTACCAA
 AAATAACAAAATAAGAGTTATGGATTATCATTTGATCTCTACATAAAGTTTCCCTTTGCAATTTATAAAAGGCAAGT

FIG. 7B (9 of 15)

AGAAAGGTATTAGGTGAGATCATGAGGTGATGTAATATTTTGATAGTTTTTCCCTAATACTCTGTGTATGCTTTTCACAG
TTTGGAAATTTTATATGTTGAATATTTATTTTGAAGTCTGTGCAAAATTCATCAAGGTCATGTGCTTTCTTATCACCTT
TCCAAATATTAGTAGTTTATACTAGTAGATAGAGAGTAGTAGAGTTTTTCAACATGAAGTTTAGCATCTTGACTTTGAAG
TAATCTAGCCAAATGACTGAATCACCCCTAGATAATGGTGAGGCCATCCTTTAGGTATCACTGGATGGCACCTGGGGTCC
TTCTGATGTGGAGCTACTCAGCTGTGGCCAGCCCGGCTCCAACCTGCCAGTGAGTGACATTTGGTCCATAATAACAACAGA
AAAGTGTAGCATGTTGTTAGAAGCAAAGCTGAAAGCATGGAGAAAAAGAGAAACAGCCTAGAGAAAGGTCAGGACAAAAG
AAACACAGGTTATAAGGGCCAAACACTAAGAAGCTCAGTCAAAGGTGCCCTCCCGATGGGATTTGGATGAACAGGAATTTG
TTTACAAGAGCCTGCAATTACCAAGCAGGACTGGGGTCTTTGAACTGCTCACAATTAACCAAGATTCACTCCTTAGG
CTTTTATTGCTTTGAATTTGTGCCCTCCTATGAGTGTAAAACCTTAAACATTTGTGTGCTTAATGGCTTCGTACACTCT
CCATCCATGCCAAAAAGACAAGAGGGTTTATCCTTACTTGACTCAAAGAAGCCATTGCCAGGGTGGCTGGGTGAGTTG
CCCCAAATTTGTTTAGCACATGAGAAAAAGAGCTAGCAATTGACCCAGTCCACTTGGTTCCCTATATTGTTTCCCCTAC
TTAGAATTAGAGGTATATATTTTATCTTCTTGTGCACTGTGATTTGCCACAATATGGGAAGGCTGGTGAATTTCCAAGTTT
CCAGGGTACAGAAGGCGAGAAGTAAAGAGTGTGATACCCAGGAGATACCTCAGCAAATATAATGATGTTAGCTGAATTA
GAGGCCAAGCATAACATCTTATAGGGAAGCATATACCAGTTGACAGTGCTATTTTTATTTTTGTCTTAGGAAATGCTGAAC
TTTGCTCATTAGTCTCAGAGGAAGTCTCAATAATCAGTGAACATCATTCTACCTTGCACTTGCTCCAACTTATTTCACTT
CCAAGAAGACAAGAGATTGCATTATGTTAAAAATAACCTTTATAAACTGTTGGTCTTCTTACCTAGGCATTTTATGGTCA
ATGTTTTGGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCTGTGGACAAAACCAAGTTGGATCCTAACAGGAT
ACAAAATTTTACAAAAGTAAAGGCTCAGCTCTAAATCCCTTCTGTTCTTACCAAGAATACCTAATGATCTCATCTATC
TGGACTCTCCAAGTCACTTAAATGCAGTCAAACCTTTTCTGCTAGAGTTCAACTACTAATTGGTCAGATCTTAAAGAAAA
TATAGTCAAAGGAGGAATCATAATAGGAGCTACCACTTATTAAGCACCAGTGTGTACCTGGAAGTGCATTAGGCCCTC
TACATACATCATTTTATTTTATCCTGCAACGACCCCTGGAAGTAGATTTTGTCTTCTATTTTAGAGATGAGAAAACCTG
AGACATGGAAGAGTCAAGCAAGTTTCAAGGTCATGCAAGCAGCAGAGCCAGTACTCAGACTTGAGGTCTGTGCTTCTGA
ACCCCTACTCTTTCAGCACTGCTCTTTACTGCTTTTATAAAACCTTTAAACTCTCCATTTCAAACCTCGACACACTTAG
TGGCTTCTCTTCTTAGGCTGCAAGTATTCCTTCCATCCAAGTCCGGGATCACTGTGCTGTTGGGGGAATGGTAAAAACGG
CTTGGGTTTGGGTTTCTCACTTTTACAAGAGGGTATGTTCCATTTTACCCCAAAATGGGTGTACAGTTCTGTATGCTAAC
ACGTGGAGGTGGTATCAGCTCCACAGGGTAAAGGCTCAGTCTCTCAAGACTGCCCTGACTTCAAGATGCCAGCTTCAA
GAGGGACCCCCAGGCCAGCCAGCTTCTGATCAGCCAGCTACAAATTTGGGAGTTTCTATAACCTGTTAGCTTGAATAA
GGAGAAAACAAAGCAATA
TTCACTACAATGACTCACAGAATTTCCAAAAAGTACTCTGGTTACTATCAGAGTATTTATGATAAAGGGTGAACATCTTTTT
GTGCCTTTATTTATGGCTTCTGGCTCATCAGTGTGTTCTCCAACAGGAAGCTCCGCCAAGTCTCAGTGTCCAGAGATT
TTGTTGGGGTTTCTATTATGTAGGCAAAATGAATACAGTCTCCAGCCCTCTCCTGTCTCCAGAGGTCATCCAGTTCTCTAC
CCTGTAATCACAGAATTGGTCTTTTGGTGGCCACTTGGCATCTCTGAAGCTATCCAGGGGCCAGCATGAGTCACCTCAT
TAGCATCACAAAGACACCCATCACTAGGAAATTTCTAAGTGTCTTCAAGCTCTGTGCTAGGAAATGGAGACAAAGACCA
GACATATTCTTTTATATACCAAGCTGATGCTGCCACTCAGCCCAACTCACATGTCCATGAATGAGCTTTCTAAGTTA
CTGGAATAGTGAAGTGAAGGTATCATTAAGGGCCCTGGGACAGAGGACCATTACCATCTAGCAAACCTATAAAATG
AAAGGTCCAAACTCCAGTTCCATCTTCCAGGATATGAAGAAGATAATGAAGAGGGGAAGAATTGGCCAAATGAAGAG
TTTGTTTTTCTACATTTTTTCAAGATGCTTCTCACTTAAGACACATTCCTTAGCCTCGGCTTGAAAGCAGTGGCTGTGGT
AAGAGTTTAACTAATCTTCAGACACACATGTCTGGGAGATGGAGTTGGCCGTGTGCCACAGTGATCTGTACATAGCACA
AGCTGTGTAAATGTGACCTCCCTCAGCCAAGGTGCCCTTTTCCCTCTTTTAAATTTCCAGGGTAGGTTGTGAGAGTT
TGGAATGAGAGTCTGAACCCAGAGTTACAACCAGATTTCTTATACTAAGTCGTGATTTACAGTCTGAGGTGAGTGACCC
CACTCATCCCTTTTCAAGTGGGTGAGTGTCCAGCATCTGAAGTCACTGAGTCACTTTTCTTCTAAGAGATTGTGCTCTTTAA
TGAGTACTTATTCGCTCTGTGTTTGGGGTGGAGGTGATGTGAGTGTGTTTAAATGAGGCCTAGGCAGTAAATTCAG
TTTTGGTGTTTAGTTCTATGAGTTTGTACAAACACATGTGACTACCTTCAATAACCAAGATATAGAACAGATCCACCACTC
CAAAATACTTCCCGTGCCCATTTGGTAGTCCATGTTGCAATAGTTCCTTCCCTTCCGTGCTGAGTAGTATTCTGTGTGT
GACTACCTCACCATTTGCTTGTAAATTTCCCACTGGAGTGACATTTGGGTTGTTTCTAGTCTTTGTATGAATAAAGTTG
CTGGAGACATTTGTGTACAGGTTTTTGTATGGACATAAGCTTTTCAATTTCTCTCTGTACACACATAGGAGTGGGGTTGCT
GGGTCCAATGGTAGTGAGTTTAACTGCATAAGAGACCGCCAGCTTCTTCTGCAAGTAGCTGTGCATTTTGCATTCCCA
CCCTCTGTGTATGACAGCTCTAGCTGATCTCCATCCTTGCCAGCACTTGATATTGTTAGTTTTCTTTAGTTCCGGCCATTC
ATGCTTCCCTCATAACTGTGAGGTAGTCATTGTCTGTTGTAAGGAAAGTTGTCTCTTTGGAATAGCAGTTTGCAAACT
CTCATACCAAGGCTTCCACTGTGGATCAGTTTGTCTGTGCTAGGAAGGTGCGGCCGGTGGCCCTCACTCTCCCCACAGGCA
CATTTCCCTCTCCCTCCTTGCAGCCCTTCTGTCTTGGGGTGGAGAGGAGGAACCTTCTGCTGGCCACATTTCTCCCTG
CATCTGTAGCTTTTCTGCACTGGGCAGGGCGGTGCGGCACGCGGTGTTCTGCTGATGCCCTCCATTGCGTCAGGGATGG
CCGTTTGCAGAATAGCTCATCTTCTCCCTCCGTGCCCTTTTCCCTTAGGCCTACATACAGATCACTTTTGTGGAGCCCT
ACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGAATTTCAACCTCCGGAGGTTTATGTACACCACC
CCGTTTACCCTGGAGGGGCGCCCTCGGGGAGAGCTGTCATGAGCAGTACAGAAGGAACACAGTCTTGCACCTATGCACGC
CTTCCCTTACATCAAGACCAGGATCAGCGTCATCCAGAAGGAGGAGGTAATGCACCCAAGGGATTGGCCACCCTGGATG
AGTGGGCTGGGTGGCCTCCAGGAGGACCCACAAACCTCTTTCACAGTGGATTGGACTGAAAACAAGGAGGGATGCATTT

FIG. 7B (10 of 15)

GAAATATGATTATATGGTTGTCCTTTCACCTCTCATAGTGCCAGAAAATCCCATTTAGGCAGCTACATATTTTATAGCACT
 ATTGTATATTAATATTTAATATTTTAAAGTTATATCTTTAGTATAAGTGTGTTATGTATTTAATTATAATATTTAATA
 TATATTTCAATTATAAACTTGTACAACAGATATATTTACCTTTTAAATATTTTATATAAAATTTTCTATATTTCAAAGC
 TTAGAGGTGATTCAAGCATAGTCGTGCTGTTAATTATTTGGAGACGGGACCTGCACGTGGGCAGCCCCAGTGAGCGGTTGG
 TGTGCTGTGGGAAAGGGCCGTGTAAGGTAGACAAGTTCACTGACTAGCTTCTAGTCCTAGCTTCCTCCTGTGATTTTAAA
 CAAGCTACGTACCTTCAGTTTCTTCATCTATGCATTAGCAGGAAAGACCTCTAAGTACAGTACAAGATTATACTCATTTT
 ATTAATAAAAGGACTGGTCAAGAAGGTCTCTCAAACCACAGAATTGTTCAAATTTCTACACACCATAAAACAATTATTAT
 TCTTTAAACACATATATACACTTATTTGTCGTCCTTTTATGCAGGGCCACAGACTTCTCTGTGACTGTGGGTTTGC
 TGATCACAAATTCAGCATTTTCTTTTATAAACACACCCGTAGTGCTTTGTCCATGATTTTCAGTTTGTGCTTGTGTAAGC
 AGAGTGAGAGCTTAAAGATCCTTGTAAACAATTTGAGAGCAGAAGCCTTCTGGATGTTTATGATGTTTTTCTCCCCGAG
 ACTTTGACAGCAGTCTGTGCACACCTAATATGACAGGAATTTTATAGCAACTCACTTTCATAATATCTTGTCCAACCA
 TTTGGCTTGGTTTTTATAGAAAGAAATCTTTTCTTTCCACACCCATGGTTCATCAGTTTCTCCATTATCTAATTAGATT
 GGGTCATTAAAATAACAAGTATAACAGGCATAATCAAGTTGGTGAACAAACACAGATGAATTGTGGTGAATATATACCTC
 ATCAGGCAGAAGCAGAAATAGCTGAGCTAAGTGGAGACTCATCCAGCAGGTAGTGTTCAGCTGGGTAAACCATCAGGCT
 GTGGCTTTTCACAGAACTGAAGAAAGCCTGAAGCAGTACTCAGTCGGGAGGAGGTGGGTTTGAAGCCATCTGCTGTAC
 TTCCTATACTTCTTGGTTTGGACTTTTGAACACTGAGACATTCTAGGCATAACACAGATATAAACTCATGGTGGCCAAAA
 GCATTTCAAACCTTTTCTTTTCTTCATTCTGCTTCTCTTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTG
 TGTCTCTGCTCTCTCTCTCTCTCTTTTCAATTTTGTAGACAGGATCTTCTCTGTGTCCTTAGAGTGCAGTGGCATGAACA
 TGGCTCACTGCAGCCTCGACCTCCTGGGCTCGAGCAATTTTCTACCTCAGCCTCCTGTGTAGCTGGGACTACAGGCTTG
 TGCCACCTTGCCAGCTAATTAAAAATACAGAGAGATATATATTTTGTAAAGAGACAGGGGTCTTACTTTGTTGGCCAGTC
 TGGTCTCAAACCTGTTGGCCTCAAACGATCTCCTACCTCAGCCTCCCAAGGTGCTGGGATTACAAGTGTGAGCCACTGCA
 CCAGCCTGAAGTTTTCTTGGCCTTCTTCTGTTCCCAACAACCTCAACAACAGTTCTCAGCTGTTTGTAGGGCTGTAGA
 ACAAGTTCCATAGACTGGGTGGCTTAAACAACCTGAAATTTACTGCTGTCACAATTTCTAGAGGCTAGAAGTTTGAATCA
 AGGTGCCAGCACTGTTGGTGCCTTCTGAGGGCTGTGAGGAAAGGGTCTGTTCCAGGCCTCTCTCCCTGACCTGTGGACAG
 CCTCTTCTCCCTGTGTCTCTTTCATCATCTTCCCTCTGTGTTCTGTGTCAGATTTCTCTCTGTAAGGACACAGT
 CATATTGACTAGGGCTTACCTGCTGGCCTCATTTTAACTTGATGCTTGTGCTTGTAAAGACCCCTATCTCCAAAGAGGTCA
 CATTCTGAGGTACTGAAGTTAGGACTTCGACATATACATTTTGGGGGAACACAATTCACCTATAAAATTCAGAAAAGA
 CTCTACCCCAAACAGCAGAACTTAGCAAAATAGATTGATTGACCTTAAAGAAATTCATTTACTGAAATTCACCCCTCA
 GTTGGAGAAGGCACAGGTGATATCAAAAGCCTGTGTTATGATGGGGAGAAAATCTTGAGTGCTGTGCTTCTACTACAGC
 TTTCTGCATTGTAAGTTGAGTAACATGAGGCTGTGTGCGGTGGCTTGTGCTGTAATCCAGCACTTTGGGAGGCCGAGG
 CAGGGGGATTGCCCTAAGGTTGGGAGTTTGAAGACAGCCTGGCCAAACATAGAGAAACCGCATCTCTACTAAAAATACAAAA
 TTATCTGGGTGTGGTGGTGCATGCCGTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGG
 CGGAGATTGCACTGAGCCAAGATCATGCCATTGCACTCCAGCCTAGACAACAAGAGCAAACTCCATCTCAAATAAATAA
 ATAAATAAATAAGTAAGTTGAGTAACCTTGCTCAGTAATAGGAAAGGCACCTGACAGGGTAGAAAAAACATGGACTTTGA
 AGATAGACATACTTGTGATCGAATTATGACCTCCTCCCTTACTACCTGTGGCATTCTGTGGAACCTTAACCTTACAAATCC
 CCTTTGACTGTAAAAATGGAGAGTATAAAGAGGTTGTTGAGAGGAATAAATGCTAAATGTATGTAAGTTTCTTGGAAACAT
 AAGGAATCAAGAAATGTTAGGCCATCTTTCTTTTAACTGTTAAGAGTATTTTAAATTACTCTGAAAGTCTTTCCCTA
 GCTGCCCTCTCAAATTCAGGTGGCCTCTCTGTCTAGCTCCAGGCTTGTCCATAGCTTATGAGACCAGACAGTACTTCC
 CTATGTTTACGTCTCATGTTTCACTTTGTTTGTGACACCGATTGAAGTTGCCATTGAAGACATGAAGAAGAAGACCTGCAG
 TTAGCAGTTGCCATTAACAGGAGCCGCTGATGCAAGATGCTTCAGATGGTGCTGCAAGGCTCTGTGGGAGCTACTGT
 AAATCAGGTAAGCAAAACAGAGGTGGCAGCTCCTCTGGTTCTTATTATTTAGGTTGTCATTATACGTCTGCACCCCTTCT
 TCCTTGGGGTTGATGAGGACTTTGATCCATAGACAAACACAGAAATGTTTCTACACTTAACCTGAACACCTGTAAGGTTT
 AGAAGACTTTTAGGAAACCTCTTCCCTTTTCAATGTAACAACCCAGGTAAAAAGAAATCTTAGAGATGAGTGGACAGGC
 TTTAAGGAGTACCCTTTCTCAGAGGAGTCTCCACTTCGGGGCCAGACCTGACAATATGATGCAATCTGGAGTCATGTT
 GAAGAATGCTTAGTCATGACCAATTCACGCAGAGTAATTGCAGGGCTTGAGACTCACCTACAAATGCCTATAGGAGAGAA
 GGAAGAGATCTAGAACATCCAACCTTTGGCTCAGTCAGCAGATGAACCCAGCATGCCAAGGACCTTGACAACAGGAAT
 GACCTGGGACCTGACTTCTTAGGCTACTTCAGACAAGACTAGATCTTCTATCAGACTTCTTGAACGCTGACTCCCAAG
 TTCAGCATGGTGCTCAAGCAGTCTCAGATGAAGGGAGGTACCAGCCTAATACCTCTGTCCAGTGGGCTCCTTAATTCAA
 ATCTAGATCTGTTCTGTCCACACTTCCACGGCAGTTATTAGTGAGCATCATGAGTCTTTCTCATTCAGCGTAATTGG
 ATTTCCCCACAAAAGTTCTGAGTGTACTTGACATCAAGGGAGCAGAAACAGAGAAGAGAAATGCCTATTACATTTCCCAAG
 ATCAGGAAAAAAATGAGGAAACGTTTGCCTTTGTAAGTGCCAATCCTTTGATAAAATGGAAGACTTTCCAAGCCACA
 ACCATGGTCTATCTTACACGATGGATATCTGACTCAATCCAGCAGTTATGCAAAATGATGTTTGGCCATGAAGGCAAC
 TAGATAAGTGAACAAAAATGAATAGATCAAGGCAATCCTGATTTTTAGAAAAGCAACTCAAAGCACATACCATTGATGT
 AGTTGTATTACACTTATATATGAATGAAAATCTATTATTAGTAGTATTTGATTGATAAAATAATATTCGGCGCCAGGCTC
 AGTGGCTCATGCCTATAATCCCAGCACTGTGGGAGGCCGAGGTGGGTGAATCACTTGAGGTGAGGAGTTTCAAGCCAGCC
 TGGCCAACATGGTGAACCCCATCTCTGCTAAAAATACAAAAATTAGCCAGTGTGGTGGCAGGCGCTGTAGTCCCAGTA
 CTTGGGAGGCTGAGGCAGGAGAATCCCTTGAACCCGGGAGGTGGAGGTTGTAGTGAGCTGAGATTATGCCACTGCGCTCC

FIG. 7B (11 of 15)

TATGTGAGAACAAAAAAGCAACATGCTCAAACCTGCTGCACCTTGAACCAACTATAGACGTCAGTTCATCCATTCA
TTCAGCAGTTATTGAGCTCCTACTTTGTGCCAGGCACTGTGCTACATATGTGGAAGGATGAAGTCCCAATATCAGTAGGA
CAAGGCTACAGACAAAACAGTACTGCTGCTCATTATTCATCTCTATGTGCAAAACACAACAGATGGCCTGCCCTCCACTTC
ATTCTACAGAGATCAGAAGTCGTGGGTGAGAGTGTGCTGATGGTGCACAACCTGTGTAAATTACTAAAACCTCATCAAACCTC
TAAACATAAAATGGGTGAATGTACGGTATGTAAATCATACCTGAATACAGATAGTAGATGAGGTTCTCTGTTGCTTA
ATTGCTTCTCAAGTCCAATCTGGAAGTTACAGCTTTTAATGAATAGAGTAACTATTTTTTTCAGGTTGTTTGTGCTGTGTA
TTTTCTCTCCACTCTGCTAACAGACAGCAGAGGTGACGCAGAAAGTGGAAAATATTTGGGGCTTGAACAGCTCTCAGGTT
TCCCCTTTAGTAAGCTCCAGCTTCTCAGCAGACTTGGGCTGTAGATCGATAAGCCCAGATTTCCAAGTGACCATAAATG
AGTCTCTGTTGCTGAGAGCTAATAGCGGAAACATTTGCTTGCCAGGTCCACTGCGTCTAGTGCCACCACGGGGCAGCGAC
CTTTCTGACTCAGCTGTAGTGAAGCAGAAACAGCCATAAAGAATCCTGGCAGCCTGATTTGCTGCGAGCCAGTACTCATC
CAGCCAGTCTGCAACTCTTCAAACCTGTTACCAAGCTGGGACCTCAATCAGCTTCTGTCTTTTCTGCAATAATAAAAAA
CATCTCGGGTTTCAAGCCAAAGACAAGAAGATAGAGAGATACAATCTTCTATCTTCTCTCTGCTCCCCCAACACCCC
GACCATTTAGATTTTAAATTTTCTTCTTATACTTTATCTGGAATTTCTCATCTTTATAAAGACTAAGTGATGTTAAAT
TGTTTTTAATTTAAATAAAGATAGTAGTACTCACTGGCACCAGTTACAGCTTGCCTTTAAAGAGAAGTAGTTTCAGATAC
ACCCTGAAAGGGTTCTGCAGCATATATGTGGTCATAGGCTCAGAAAACAGGCTGTTGAGTGGTGGCGTTTAAACTGGA
GTTGGGGTCTATGAAGAGGAAGGAGAAGGAATTTGTCGAGTAGCCAAAGGACAACCAATGTGTAGAGTGTAGGTGGAA
AAAGAAGCAGTAGTTTAACTTGAGACCAAGGCCATATGCCTGGCTTATAGCTGGAAATGGGGAATGGCTTTCTAGGC
AGTATATGTGGCGTTGGGGTTGGGAATATGGGCACCTCAAGCCAGATTTGCCTGAGTTCAGATCCCATTCTGCCTCAACTAG
ATGTGTGACCCCTGAGAAGTTACCTACCCTCGGTTTCCCCAGATGTAAATCGGAATAATAATTGTACCTCTCCCTTGCAG
TTAGTGACAGAATAAAATGAGTTAATACATGGAACCTAGAATAAGACTTCATACATACTAAGGGATCAGTAAGTGAACA
TTGTTTCAGTGGGGCAATAGGGGACTGATGGATTTGAGTGGGAAATAGAGAATTAATCTGACTTAAATACGGAGATTGTC
TATCCATGATTTGTCTGTCTCTATAAAGTTTGAATCATAGACACAGTGATGCTGATGAGACATTTGGCCTGGGAGCAGCA
GGATTTCTGGGTTTATATCCAGCTGTGCTGTCCCACAGGTATGTGACTGGACAGGGCACTTCACCTCTTGCATGTTAGTT
TCATCAACTATGAAATAAAGAGACTAGAATACAGCATCTCTAATAGTTTATCATTCTCATATTGTACAAATAGTTCATTT
ACTTAGCCTGGGTCTGTGAGGCATAATAACGCTACCATGTGCTCTGGCTTCAGCTGTGTGCAGGGACTCTTCTGAACATT
TGATATGTTTCAACTAATTTAATCTTTACATTAATTTATGAGGTAGGCTCTTATCACCCACACATCAGATGAAGAAAC
TATGACATGAAGAGGTTAAGTAGCTTGTTTAAAGGTTGCAAAGCCAGTAAGCAGCAAAGCGGGATTCAAGAGTTGAGCACTC
TGGCTCCAGAGTCCATCCTCTTAATTGCCATGCTGAGCTGTTCCCTCTAGTGACTATATTCAGTTGCTAGTAACAGAAGG
AAGAGTAGCTTAAATAAGAAATTTATTTTCTCTCACATTAATAAGATTGGAGGTAGTCGATGTAGAGCTGTGTAGTGG
CCTCATAAAGTCATCAGAGACCCTGGTCTTTTCCAATCCTTTGCCATGCCATCCTGGTTCTAGTGTACCCATTCTCGTG
GTCATGATATGGTTGCTAGGGCTCCAGCCATCATGACCACATCTAGGCAAGTCAGGAGTAGAAATGAGGAAACAGCAAAA
AGATGTGCCCATTTCCAGTGCCCTTACCTATATTATCAGCGATCCCTACCTGCATGGGAGGCTAGGAAGTGTAGTGT
CAGGTGGTCACACTGCTGGAGTTCTGCCAGTAGGGAAGAAAGATGGATATTGAGAAAACAATAACGAATGTTTGTCT
GCCACACTGAGGAACCCATGTATGGGCTGTGCTGAAAAGGGGGGCCAAGGCTGGGTACAGTGGCTACGCTGTAAATCCC
AGTACTTTGGGAGGCTGAGGTGGCGGATCACTTGAGCTCACAAGTTTCGAGAGCCAGCCTGGGCAACATGGCAAAACCTCG
TCTTTACAAAAAATACAAAAAAATTAACCGGGTGTAGTGGCGTGCCTGTAGTTCCAAGTCTCGGGAAGCTGAGGTGGG
AGGATCACTTGAGCCAGGAGGAGAGGTTGCAGTGAGCTGAGATCATGCCACTGCCTTCCACCCTGCATGACAGAATGA
GATCCTCTCTCTAAAAATAGAGGGGGTACCAAGAGATGCAGGGGGGGTGAGGGCAGCATGACTACTCTCTGTAGGAGA
CCTTAACCTCTATAAATGGAGGCCCAAAATGTTACTGCCATCAAAGCCAGGAATCCTTTTCTGGAGGCGTAACCTCCTG
CCCTTTCTAATCCCTATCAATCTGGTTTCTGTAGAAGTGTGACTGTAGAAAACCCAGGCATATTTGTTCTAAGAAAAT
ACTTGTGTTCCGTGAATTTACCAACAAAGGGAGCATCAGAGGATGTGAGGGAAGTCTGGAATGGTTGTATCACTAAGTGA
GAGCAGCACAGATGTTTGTGGACCTATTGAGAATGTTACAGATAAGACCATTTTGAAGAGTTGTTTGCAGTGTCAATTT
ATGATCTTGTGTACATTTTCCAAGCGATGTGGCTATTCTCTAGGAGGGATAGTAGAAATTTATTTCAATTTTAAATCAAATA
ACCTAGAGAATATAACCCAAATGACTGAAAGGAAGAAATGTAGAAAAAGTATATAAAATAATTTTTTGCATTATAAAAGT
TTAAAGACATAAAGTAATATTACTACATAAAATCTAAGTTTTTTACTCCAGCTATTAATATGTTTTTCTTTATAAAACAT
CACATTTATTAATGCTGTGTAAACAACTACCTCACAATTTAGTGGCTTAAAAGAAAATTTAATTATTATGCATGTGGTA
CATAATAATTTTTGCTTTTCTTCTACTCTGATACTTGCCATGATGTGGTGTGATGGCTGGGGCCCTAGCGAGG
TGTATTGTGGCCATGAGAATGGTTTGTGCAACTTGGGGTGGCTGGGCTCAGCTAAGCAGTTTTTGGCTGGAGTCTCT
CAGTTGCACTGAGACAGTGACTAGGACTTGAATTACCTGAATGCTTCTCACTCATGTCTGGTGTCTGGGCTGAGAATAC
TCAAACAGCAGGGGCTCCTCCTCTCTAATCTCCTTCTCTCCACATGGTCTCTCCTGCATGACAGCTTTAGGGTAACCT
AGACTTGTACAGGATGGTTTCAAGACTCTTATAGTACAGAACGAGAGAGACAGAGGCCATATTACCTTTTATTAGCCA
GTCACACAGTACCACCTCCACCACATCTTATCAGTGTGGCTGTACAAAGAACCATCCACCTCTTGATGGGGGCATGGG
CAAGGTTCTAGGAGAGCACATTTCTGTGGCCATTTTCAAGAAATACAATCTGTACACTCCAGAAGCATCTGTTTGCCTTA
TTATCATAGCTTCTGATTTAATTTCTCCAGCAACCCTAGGAGATTATATGAGCTTATTATCCCCATTTTCCAGAGAAAAT
TGAAGATTTTATGGTTAAGTCATCTGCTAATGAGTAGCAGCTTGTTCACCCGAGTTGTCTGCATATAACACATTTA
ACTCAGTCAAGGGCAGATGGTGAGCAATCAGAAGGTGTAGTACGCTGCTGCTACTTCTGCAAAACAAAGACTAAGGAGAG
TTTAGCTGATTTTACCAAGTTGTCCGAGTAGACTTCCCCAATTAGCTGTTAGCTTTGGCAGGACTCATCCACCTCCT

FIG. 7B (13 of 15)

TCCGATAATGCTTTGCTTTTTTCTTATGTCACCTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAAGTTTCTTTT
 TATAAAGCAATAATATCTCTGTTTTTCATTTTCAGAACATTGTGCTGTCTGTCAGCATATGTATATCAGCTACAAAATATAT
 TCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAAGAGGAACAAAGACATTATTTGAGAATTAATTTATATATTTT
 TAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAAATGCAAGCTAAATGTTTCCCTTTGCAACTCATGCTT
 TGTGTTTTGTTTTGATGACCTACTCGCTCGTAATGTTTTGTAAGGCACTTCAGAGAGAAGACAGATGCATCATCTGGCC
 TCCATCAATAACACTATCCAAGGTGGCACCTCTTCTGCAATGTTTAACCTGCTAGTAATGAACGATGACTTAGTTCGG
 ATATTTTCAAGAACTTTTGTATATACCATCAGGTATGCATGAATTTATAATCTGAAAGAGGACTTAAAAATAAATAAAA
 CTTACCAGCTTAAGTGCTAAACTTTTTATTTTTTAGGTATTTGGGGAAGAACTCTTTTAAAGTATACACCTAACTGCTT
 TTTAAAAATGAGTACACATGACATACTTTAATTCATATGTATTCCCTACTCTTTGGGAGACACTGTGTTGAGACCAAGG
 TCAAAAAACGTGGTCACCGCCCTCCAAATCGTCTCCGTTCCTGAGGAAGATCATATACCTGTGTAGTAGCCACAGTACA
 AAACAGACTAGAACACAGCCCATAGCATGTAACCTTTTCTGACTAACTCAAGGATAGGCCAACACCTATGGTATTAGAT
 TCTGCCCTAAAACAATAAGAGTTAGATGCTAAGTTATATAGTCCTGGACCTTAACTCAAATAGCCAGAATAGCCCTAGTA
 ACCTAGAATATTCCTGATTAAATATCCCTGCTTTTAGATACCTGTTGTCCATTTGGGTTTGTTTTTTACAGTCTCTTTT
 GTACCACAGTGGATACATTTGCTTCATGAGTGCAGGAACCATGTTCACTGCTGCATTCTTACCCCTAGCCCTGCAACAAA
 CACACAAAAGATACCCAATAAATATTTGTTGATTCTACTAAATGAATGAATGATGAGTAGGCCTGCTTCTAGAAGTGCACT
 GCCAATAAGAATGTAATGCAAGCCACATATATAATTTTAAAAATTTCTAGTAGCCATATTAAAAATAATAATAGGCCAAGT
 GCAGTGGCTCATACATGTAATACCAGCAGTTTGGGAAGACCAAGGTGGGCAGATCACTTGAGCCAGGAGTTTGAGACCAG
 CCTGGGCAACATGGCTAAACCCCATCTCTACCAAAAAAGATATAAAAAATTAACCAAGTGTGGTGGCATGTGCCTGTAGT
 CCCAGCTACTCGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGAGGTTGAGGCTGCAGTGAGCCATGATCGTGTAC
 TGCACCTCTAGCCTGGGTGACAGAGTGAGACCCTGTCTCAAAAAATAATCAGCATCATAAAAAAGAAACCAGCAAAATTAAC
 TTTACTAGTATATTTAACCCAATATATATAAATATTTTCAATATGCTTCCACTATAAAAAATTTATTTACAGTCTTT
 TATTTCCATATTAAGTCTTTAAAAATCTGATGTGTAGTTTGTACTTACAGCACGTTGCAGTTAGGACTGGCCACATTTTA
 AGTGCACAGTAGCCACAGGGGGCCACTGGCTACCATATTGGATAGTGCCATTCTAGAAGCTTTCAGCTTTTCAACTGGA
 TGCCTCTGATTTGTGGACTCAGAATACAGATAACCAAAGAAGTGGGACTAGTGTCTGAAGTAAGAATGACAGGGTATGAT
 TGAGAGCCCCATGAGCTTACCTAGGAGAGAACTTGTGGGTTGCAGAATAAGGATTTGTCAATATTGGCTCTAGCTGTT
 CACACTATTTCTGGGCAACTCCAGATCATTTCTCAACTCCAGATAGTTAAGTGGGGAGCATGGCTGCACTTTTTTAAAG
 TGATGGCACAAAAAAGATATTGAACGTTGGTCTCTGATTATATATTCTAAATATGCAGTTAGAAAAGAGGCCTTTTAA
 GAATCCCTAAGAGTAAAGCAAATTAGTATCTTTGTTTCTGAAAATTAGAGAACTTGATATGCCATGATAGCCCTCTTC
 ATTTTATTTGGAAAACCTCTTCTATGAAAGCTTATTAGAGAAAATTTCTGATTAGCTTCATGCCTCCCTCTCTTCAGCAA
 GGTCAAGGGTGCAGTTGTCACTATCACATAAGAATCTCATAAAAAATTAACATGAATATACTGCACAGATCTGATTGGGT
 TTGTCTATGCCACACATTGTTTTAAATTCCTAATTCTATTTCTATAAAGAGTGTTTCTATGACAAATAGATCGTTTTAAAA
 ACAACAAACAAACAAAATTTAGAGTTGTCAATTGGTAATTGTGGTTGCAAGTATGCTTTCAAAGACCAGAAGCTTTTGT
 TTGCTTTGAATGTAATTTTTTCTTTTTTCTTTTTGATACGGAGTCTCACTCTGTTGCCAGGCTGGAGTGCATTGGCAC
 CATCTCAGCTCACTGCAACCTCCACCTCCGTGGTTCAAGCAATTCCTGCCTCAGCTCCTGAGTAGCTGGGATTACAG
 GCGTCCACCACCAGCTGACTAATTTTTGTATTTTGTAGAGATGGGGTTTTACCATGTTGGCCAAGCTGGTCTCAAA
 TTCTTGACCTCAGGTGATCCACCTGCCTCTGCCTCCCAAAGTGCTG

FIG. 7B (15 of 15)

GGAACAATTTCTCTCATGTGTATGGCTCCCTAAAGTGTGGCTGAGCATTGTCCACATGGGTG
 ATGCAAAGGATCACTGAACTAGGAGCAGTTGGGAAAAATACAATCATTTGGGAATTCCTGTAGC
 ATCGAATGTGCTACAGGGAGGTAGAAGTATTCATACAACAGTTCTCTGGTGTTCCTGTGTA
 GCAACCAGTCAGCCAAAAGGGTTCAGCTGCTTGAATGAGAATGGCTGGATCAAAATGGCAGCT
 CATGATTTAAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAACCTCTGAATGGCTG
 GGGGAGAAGGAGTCAAATGCCCTGGATCTTTTCTTGGGCCTCAAAGTCTCTCTGTCTATCA
 TCCTTCCAGTATTGGGCAGGACCTGACTGCAGGCATCATGGCCTCTGTGAACCTCTCAAGGGTA
 TGTATTATCTGACAAAACCTACGATGTCCACTAACAGGCCACTGAAAGGTATCTTAGTCAGTTC
 TGCTCATTGCCAGCCAAGGCCTACGTTTTATAACATGATATCAAAGATTGCATCTAAAATTGT
 GATGATTTTCCATAAATAATCATTTTCATTTAGATTTTTCTATTTTAAATCCAAGGTATCTTCAGC
 GGAAATAAGGAAACAGTTTACTCTCCACCAAACCTTGGCCAGTACCATCGACAGAGCATAAGT
 ACCTCTGGCTTCCCTCTCTTCACTAGTAAGTATGAGTTCAGGTTTACTTAGCGATTGGTCA
 AGTGCAAAAGTGCCAGGGTATGTGTTGCTCCTGTTCCTTAGATCTTCTACCATCACCTCA
 CATCTCCAGTCACCAGATCCTAATCTGTGACTGTGTCTGGACATCAGACAATATCCCTCTCT
 CTCTCTGCCAACCGGTACTTAGGGTACATAATAGAACCCTCTGGGAGCTGTGGTTTTGATGTCTC
 TAGACTAGGTGGGCTTCCAGGTGACTCAGTCTCATCCAATTATGGTTCATATTTGGGGGAGAA
 GGGCTAGCCCAAAAACCTTACCACCATTTGTAGTATGCATTTTTTTGGAAAAGCATATTCCAAAA
 TCTGAAATGCCAAGTTACAGACCTCCTTTTTGTAAAATAATTTCTTGCTAGTATAATTTACAT
 ATAATAAAATTCACACATTTTAGGTGTACAATTTGGTGAACCTTGGGCAACTTAGAGTCACCTAA
 CCTTTCCTCAGTCAAGATATAGAACCTTCTTTTATCCTAAAGCGTTCCCCAGCGCGCTTTTAC
 AATCTCCTCTCCCCAGGCCACACCTCCAACCTCACGCAATCTCTGACTCACTTCTGTCAACATA
 ATTTTGCTCTATCTGGAGCTTCATATCCTGTTACAGTATGTACAAACCTTCTTTTTTTGAGACA
 GGGTGTCTAGTCTGTCAACCAGCCTGGAGTACAGAGGTGTGATCTCAGCTCACTGCAACCTCAAC
 CTCCCAGGATCAGATGATCTCCTCCACCTCATCCTCCCAAGTAGCCGGGACTACAGGCGCAT
 GCCACCACACCTGGCTAATTTTTGTACTTTTTGTAGAGACAGGGGTCTCGCTATGTTGCCAGG
 CTGGTCTTGAACCTCTGGGCTCAAGCGATCCTCCTGCCTCAGCCTCCCAAAGTGTGGGATTAC
 AGTGAGCCACTGCACCTGGCCCTAAACCTTCATTTTTTAAACACATTTCTCTTAAATTGAAGA
 TTGCCTACATTTTTATATCAATGCCAATTGTTGAGTGTGCCTATATGTGTTATATTTTGAAGC
 ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGGTTTTGTAAACCAGC
 AGTGAATATTCACCTCCTCTGTGAGAGAGCTCCAGCCCTCCTGTACTCACTTCTCTCACACAGCA
 CAGCAGCACTCTTGCTGGTCTGCTGCTTATCTTGAAGAGGTAGGTTACTTTTTGTTTCTACT
 TATTACTTCGAAACCACTTCTGCCTTAGAAATTTGTAAACCTTCCGCTCAGTTTTCCGGTAACCG
 CCAATTTGTCTCCTGTAACAATTTACGCGCGGTGTAACCTGTGAATCTTT

FIG. 7C

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hCLASP4 -----MFPMEDISISVIGRQRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPAKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQHWVNYK 120
      . . .

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDLDVVFTPKECRTLP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLQLPRECRTEP-GIPKD-EKLDQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSSHFEIDHEDADKDEDTSHSSSKGGGGAGGTGVFKSG 180
      . . . * . . .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQREKQKG-LPRQVFEQDASGDERSGPEDSNDSSRRSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKRRYFOLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSCT 239
      . . . * . . .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AETE QEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRLSLQPDKRL ENLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME E WITL NKILQLN-----FEAMQE K 219
hCLASP7 EDTPRSSGASSI FDLRNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNLDLTYFVLA AETESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * . . . . .

hCLASP4 TAQDDETSS---QGKAENIMASLERSMHP ELMKYGRETEQLNKL SRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD---EEDAVEIRPV ECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD---EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD---EQSKLEGGSGGLDSYLP ELAKSAREAEIK---LKSESRVKLFYLDPD 272
hCLASP7 LLTLYPAPD---EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE 273
hCLASP1 TDLGLDSLDSV TCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD 359
      . . . . .

hCLASP4 VQR LDFS---GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS---IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS---LALYDVKEKKKISENFYFDLNS EQMKGLLRPHVP PAAITTLARS AIFSI 333
hCLASP2 AQK LDFS---SAEPEVKS-FEEKFGKRILVKCNDSL SNLQCCVAENE EGPTNVEPFFV 327
hCLASP7 IEPIFGI---LALYDVREKKKISENFYFDLNSDSMKGLLRAGHGT HPAISTLARS AIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKAAKRIM ICKALNSNLQGCVTENENDPITNIEPFFV 419
      . . . . . * .

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FIG. 8 (1 of 6)

hCLASP4	FKSHLESTIYTQDLHVHKKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFQYQCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREKQ-----MSQSPTSINFIRSCKNLLNVE	887
	.. *:: ** ::. ** : :.	
hCLASP4	ETQVMIQFLPVILMQFLR-----VLTNMTMTH-----EDDVP	824
hCLASP5	RIEPLVLFHLVLDKLFQLSVQPMVIAGQTANFSQFASFESVVAIANSLHNSKDLQSKDHG	775
hCLASP3	QIEPVVRFLHLLLDKLI LLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQFLR-----VLT-RAT-----QEEVA	816
hCLASP7	SHEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVSVLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQFLK-----VLVQNE-----EDEIT	916
	. : : * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVHYVFERLPEVQRDVPKSGAPTALLDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLRNRSRLSN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPLPDGAPP----VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . : . . .	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNCRMSYCYSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLA VAPGSVDDEVSRILASKLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVCSGVSRESALQQA WFFFEIIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVWSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
	. * . . : ***	
Cadherin Cleavage		
hCLASP4	ATYLLLEENKIKLRFGRFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEHRRTRFSDRFMDDDTTIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAERKSRFPFERFMDDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQHLENSKVKLIRNQRFPASYHHAETVVNMLMPHITQKFGDNPEA---SKNANHS LAF	956
hCLASP7	ALHLLGQRLDTRKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLDITNKIQLRPQRFPEQYQNELDNLMVVLSDHVIWKYKDALEE---TRRATHSVAR	1052
	. : : . : * ** . : . : : * : *	
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP----KVLAEYKFEFLQTICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---PTLISMRLEFLRILCSHEHYIPLNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRILCSHEHYIPLNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSLLSLVDRGFVESLVRAYHKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYIPLNL	1059
hCLASP1	FLKRCFTFMDRGCFVKMNNYISMFSGDL----KTLQYKFDLQEVQCHEHFIPCL	1107
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FIG. 8 (3 of 6)

Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLRETSI 1060

hCLASP5 FFMNADTAPTSP--CPSISSQNSSSCSSFQDKIASMFDLTSEYRQQHFLTGLLFTELAA 1085

hCLASP3 PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPPRQQHYLAGIVLTELAV 1196

hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGLLREVT 1052

hCLASP7 PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGILLTELAL 1119

hCLASP1 PIRSANIPDPLTP-----SES-----TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF 1157

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hCLASP4 ALQDN----YETRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLFPVGLLENIQRL 1116

hCLASP5 ALDAEGEGISKVQRKAVSAIHSLSSHDLDPRCVKPEVKVKIAALYPLVGIILDALP-- 1143

hCLASP3 ILDPDAEGLFGLHKKVINMVHNLSSHSDSPRYSDFQIKARVAMLYPLIGIIMETVP-- 1254

hCLASP2 ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLLENVQRI 1108

hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYPLLSIARDTLP-- 1177

hCLASP1 ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAIASLYMPLYGMLLDNMPRI 1213

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hCLASP4 AGRDTLYSCA-----AMPN-S----ASRDEFFPCGFTSPANRGSSTDKDTAYGS 1160

hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162

hCLASP3 -----QLY-----DFTETHNQGRGPICATDD-- 1276

hCLASP2 NVRDVSPFPVNAAGMTVKDESALPA--VNPLVTPQKGSTLNSLHKDLGAIISGIASPYTT 1167

hCLASP7 -----RLH-----DFAEGPGQSRSLASMLDSDTE 1201

hCLASP1 YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSDKVLSIAAFSSIAIS 1273

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hCLASP4 FQ-NGHGIKREDSRGSLLIPEGATGFPDQNGTGEN-----TRQSSSTRSSVSQYNRLDQYE 1213

hCLASP5 -----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208

hCLASP3 -----YESESGSMISQTVAMAIAGTSVPQLTR---PGSFLLTSTSGRQHTTSAES 1324

hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSE 1227

hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAGSR---ASISQGPPTASRAGCALSAES 1249

hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327

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hCLASP4 TRSLLMCYLYIVKMISEDTLLTYWNKVPQELINILILEVCLFHFYRMGKRNIARVHDA 1273

hCLASP5 TRNLMICFLWIMKNADQSLRKWIADLPSTQLNRILDLLFICVLCFEYKKGKQSSDKVSTQ 1268

hCLASP3 SRSLICLLWVLKNADETVLQKWFTDLVSVLQNLRLDLLYLVCVSCFEYKKGKVFERNNSL 1384

hCLASP2 IKSLLMCFYILKSMSDDALFTYWNKASTSELMDEFTISEVCLHQFYMGKRYIARNQEG 1287

hCLASP7 SRTLLACVLWVLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKKGKKAERINSL 1309

hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQAPSPPEVSDFFSILDVCLQNFYRLGKRNIIRKIAA 1387

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hCLASP4 WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS----- 1311

hCLASP5 VLQKSRDVKAR-----LEEALLRGEARGEMRRRAPGNDRFPGLNEN--- 1311

hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430

hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS----- 1323

hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN----- 1350

hCLASP1 AFKFVQSTQNNGTGKSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442

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hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFITQCFKTQLL 1359

hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368

hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE 1489

hCLASP2 -----LTFNHSYGHSDADVHLQSLLEANIATEVCLTALDTLSLETLAFKNQLL 1371

hCLASP7 --VRWRKSVTHWKQTSRDRVDTKDEMEHEALVEGNLATEASLVVLDLTLIIVQTVM-LSE 1407

hCLASP1 --ALSNPKLLQMLDNTMTSNSNEIDIVVHVDTEANIATEGCLTILDVLSLTQTQHQRLQ 1500

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FIG. 8 (4 of 6)

hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCQSTTYLTHCFATLRALIAKFGDLLFEEVEQCFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHC FATQ RALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQ RALVSKFPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATA LKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCSSTIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSSSLVGT SQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGNNFARVKMQVTMSLSLVGT TQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
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hCLASP4 SRFQESLFIINN FANS DRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMPFPPTQVEELLCNLNSILYD TVK MREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEDLLELRETTFPDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDL 1664
hCLASP2 TRFQQSLSIINN CANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEDMGLRSTFAEQVQDLMFNLMILTDTVKMKHEQEDPEMLIDL 1582
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679
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transmembrane
hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKN GDLSEAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNM AEKHTKKKCYTEAMCLVHAAALVAEYI SMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSESRNHAEAAQCLVHSAALVAEYI SMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAMCYVHV TALVAEYI TRKG----- 1604
hCLASP7 YRIARGYQGSPDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAMCYIHIAALIAEYI KRKG YWKVEKI 1739
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hCLASP4 -----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDE DGV 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDV VSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDE EASMMEDVGMQD----- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISD DILSPDEEGF 1672
hCLASP1 CTASLLSE DTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD----- 1795
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ITAM
hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEIISEISK LIVPIYEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASFMSMAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWK SERYELIADV NKP IIAVFEKQ RDFKKLS DLYYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKKRL LGTFFRVAFYQGSEFEEDGKEYIYKEPKLTGLSEISRLVKLYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFEG-SKFGDLDEQE FVYKEPAITKLP EISHRLEA FYG 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFYG-TKFGDLDEQE FVYKEPAITKLA EISHRLEGFYG 1872
hCLASP2 ---DFEDEDGKEYIYKEPKLTPLSEISQRLLKLYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYG-AHFGDLDEQE FVYKEPSITKLA EISHRLEEFYT 1791
hCLASP1 SYLKVAEVVNSEKRLFGRIYRVAFYQGSEFEEDGKEYIYKEPKLTGLSEISQRLLKLYA 1912
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FIG. 8 (5 of 6)

